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                                                                                                                     May 24, 2004, 19:05:42; Search time 51 Seconds (without alignments) 626.037 Million cell updates/sec
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Abg24250 N
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Streptomy	App76681	ABP76681	9	19938	12.5	70	<b>ል</b> ር) -
Propionib	ADm40680	ABM40680	9	401	12.5	7.0	44
Propionib	Aau44161	AAU44161	4	401	12,5	70	43
Propionib	Abn65566	ABM65566	9	377	12.5	70	42
Protein e	Abu35653	ABU35653	9	1292	12.6	70.5	41
N. mening	Abu06030	ABU06030	9	425	12.6	70.5	40
Staphyloc	Abm71198	ABM71198	9	282	12,6	70.5	39
S. aureus	Aaw73375	AAW73375	~	282	12.6	70.5	38
Bifidobac	Abp66214	ABP66214	Ŋ	267	12.7	71	37
Bacillus	Aar50955	AARS0955	N	1228	12.7	71.5	36
Bacillus	Aau02092	AAU02092	4	1217	12.7	71.5	35
Bacillus	Aau02094	AAU02094	4	1209	12.7	71.5	34
Bacillus	Aau02093	AAU02093	4	1208	12.7	71.5	33
B. sphaer	Aar75409	AAR75409	7	340	12.8	72	32
Insectici	Aar41019	AAR41019	~	340	12.8	72	31
C-termina	Aar14528	AAR14528	7	340	12.8	72	30
Alloiococ	Adb12369	ADB12369	9	109	12.8	72	29
Chimeric	Aay31990	AAY31990	7	1227	12.9	72.5	28
Protein e	Abu25143	ABU25143	9	141	12.9	72.5	27
Novel hum	Abg21490	ABG21490	4	639	13.0	73	56

Ą AAB69495 standard; protein; 113 AAB69495; RESULT 1

ALIGNMENTS

(first entry) 23-APR-2001 

Arabidopsis thaliana PII protein.

Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.

Arabidopsis thaliana

US6177275-B1

23-JAN-2001

97US-00899330. 23-JUL-1997;

96US-0022328P 24-JUL-1996;

Lam H, Hsieh M; (UYNY ) UNIV NEW YORK STATE. Coruzzi GM,

WPI; 2001-158572/16. N-PSDB; AAF58581, AAF58583.

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 1; Fig 1; 35pp; English

The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

Sequence 113 AA;

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Synechococcus; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                          Synechococcus strain PCC 7942 PII protein.
                                   AAB69503 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                             (UKNY ) UNIV NEW YORK STATE.
                                                                                                                                                                      Synechococcus sp.
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                                                1 FYKVBAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKV
                                                                  1 FYKVEAIVRPWRIQQVSSALLKIGIRGVIVSDVRGFGAQGGSTERHGGSEFSRDKFVAKV
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                         Gaps
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                                                                                                                                                                                                                                                                                  Castor bean, PII, plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
Length 113;
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100.0%; Score 561; DB 4;
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ive 0; Mismatches 0;
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Pred. No. 6.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-158572/16.
N-PSDB; AAF58582, AAF58584.
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                            Matches 113; Conservative
                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 102; Conserv
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         Ricinus communis.
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                                                                                                                                                                                                                                                                                                                                                US6177275-B1.
                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1997;
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                                                                                                                                                                                                                                     23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coruzzi GM,
                                                                                                                                                                                                             AAB69496;
                                                                                                                                                            RESULT 2
AAB69496
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97US-00899330.

96US-0022328P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present sequence is encoded by a nitrogen regulatory PII gene. Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%; Score 312.5; DB 4; Length 56.4%; Pred. No. 3.7e-31; rive 23; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; infection; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N. gonorrhoeae amino acid sequence SEQ ID 4634.
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                                                                                                                                                                                                                                                                        Example, Fig 1, 35pp, English.
Hsieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                  WPI; 2001-158572/16
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   Coruzzi GM,
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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitroger assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII mucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KVBAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSBFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is encoded by a nitrogen regulatory PII gene. Movel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in
                                                    Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PII; plant nitrogen regulatory gene; P transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          .3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%; Score 287.5; 49.1%; Pred. No. 5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB69497 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae PII protein.
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                                                                                                                                Example; Fig 1; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitrogen assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lam H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PI; 2001-158572/16.
                  WPI; 2001-158572/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KVBAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSBFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Azospirillum brasiliense; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                          New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%; Score 308.5; DB 6; 55.5%; Pred. No. 1.3e-30;
                                                                                                                                                                                                                              Monaci E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 528; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Azospirillum brasiliense PII protein.
                                                                                                                                                                                                                              Masignani V,
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                                                                                                              12-FEB-2002; 2002WO-IB002069.
                                                                                                                                                    12-FEB-2001; 2001GB-00003424
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(first entry)
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                                                                                                                                                                                                                              Pizza M,
Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                  WPI; 2003-058415/05
N-PSDB; ABZ40022.
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                                                                                                                                                                                          CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121 AA;
                                    WO200279243-A2
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                                                                                                                                                                                                                              Fontana MR,
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23-APR-2001
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Gaps

63 ELVVKKDQVESVINTLIEGARTGELGDGKIFVLPVSDVIRVRTGERGEKA 112

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transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                 3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKW 62
                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                        63 ELVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                             50.7%; Score 284.5; DB 4; Length 112; 50.9%; Pred. No. 1.3e-27; ive 27; Mismatches 26; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli, PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69498 standard; protein; 112 AA
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                                                                                                                              Sequence 112 AA;
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                                                                                                                                                              Query Match
Best Local S
Matches 56
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform sacroharides and organic acids, nucleic acids, vitamins, saccharides and organic acids, mich particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VEALVREWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoi
                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.
62 BIVVPDDIVDTCVDTIIRTAQTGKIGDGKIFVFDVARVIRIRTGBEDDAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 IVVKKDQVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 29; SEQ ID NO 6980; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.6%; Score 278.5; DB %, Pred. No. 7.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ando S, Hayashi M,
da M, Ozaki A;
                                                                                                                                                                                           C glutamicum protein fragment SEQ ID NO:
                                                                                               AAG93226 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizoguchi H, Ando Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000EP-00127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                               Corynebacterium glutamicum.
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                                                                                                                                                                                               organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH68445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
                                                                                                                                                                                                                                                                                                              EP1108790-A2
                                                                                                                                                              26-SEP-2001
                                                                                                                                                                                                                                                                                                                                              20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa S,
Tateishi N,
                                                                                                                                 AAG93226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                RESULT 8
                                                                                   AAG93226
                                                                                                                요
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Gaps

1;

50.7%; Score 284.5; DB 4; Length 112; 50.9%; Pred. No. 1.3e-27; Live 27; Mismatches 26; Indels 1

Local Similarity 50.9

Query Match Best Local S Matches Sé

AAB69502;

AAB69502

a

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New Acinetobacter baumanni proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium leguminosarum; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 IVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 IAISDEMVDAVIESITRVASTGKIGDGKIFVTNLEQVIRIRTGETGPDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.4%; Score 260.5; DB 6;
48.6%; Pred. No. 1.5e-24;
tive 23; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; SEQ ID NO 5437; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium leguminosarum PII protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB69499 standard; protein; 111
                                                                                                                                                                                           99US-00328352.
                                                                                                                                                                                                                                    98US-0088701P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00899330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                               Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium leguminosarum
                        plant biocontrol agent.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADA30024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1997;
                                                                                                                                                                                           04-JUN-1999;
                                                                                                                                                                                                                                    09-JUN-1998;
                                                                                                         US6562958-B1
                                                                                                                                                 13-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                      Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB69499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant PII (also called P-PII) mucleotide sequences have been isolated.
They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII proteins are useful for in vitro screening of herbicides. P-PII with the promoters of P-PII promoters and individual genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is encoded by a nitrogen regulatory PII gene. Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                            Rhodobacter capsulatus; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
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H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIISDAQAEEVINIIVETARIGKVGDGKVWMINIEELVRVRIGERGEAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.1%; Score 264.5; DB 4
48.2%; Pred, No. 4.2e-25;
tive 25; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter baumannii protein #1311.
                                                                                                                                                                                                                                  Rhodobacter capsulatus PII protein.
                                                                                                       AAB69502 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA34150 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 1; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00899330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0022328P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Conservative
                                                                                                                                                                                                                                                                                                                                       Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lam H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coruzzi GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
                                                                                                                                                                                        23-APR-2001
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ADA34150;

XEXEXEX

ADA34150

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Matches

63

Gaps

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Length 124; Indess biodiversity.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                  Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIVVKKDOVESVINTIIEGARIGEGIGDGKIFVLPVSDVIRVRIGERG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                             27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 257; DB 4; 47.7%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #24245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG24254 standard; protein; 160
                                                                                                                                                                                Example, Fig 1, 35pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT
                                                            Hsieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631
96US-0022328P
                              (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
N-PSDB; AAS88441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                            Lam H,
                                                                                         WPI; 2001-158572/16.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WC200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
   24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2002
                                                              Coruzzi GM,
                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG24254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent movel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format directly from MIDO at the printed specification, but was obtained in electronic format directly from MIDO at Everyones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.7%; Score 256.5; DB 4; Length 160; 45.9%; Pred. No. 6.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Mismatches
                                  Claim 20; SEQ ID NO 54613; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum PII protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB69500 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00899330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-002232BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobíum japonicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPI; 2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS6177275-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                             31-AUG-1999;
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                                                                                                                                                                                   enzymes.
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                            The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                      3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                   3 KIEALIXPFKLDEVRS-LSGVGLQGITVTEAKGFGRQKGHTDLYRGAEYIVD-FLPKVKI 60
                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum HA protein sequence SEQ ID NO:318
                                                                                                                                                                                                                                                 63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERG 109
                                                                                                                                                                                                                                                              EIVIGDDLYERAIDAIRRAAQTGRIGDGKIFVSNIEEAIRIRFGESG 107
                                                                                                                                                           Length 111;
                                                                                                                                                                                 28; Indels
                                                                                                                                                           45.6%; Score 256; DB 4;
47.7%; Pred. No. 4.9e-24;
tive 26; Mismatches 28;
                                                                                                                                                                                                                                                                                                                           AAB79181 standard; protein; 89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DE-01032928.
99DE-01032930.
99DE-01032933.
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99DS-01032127.
99DS-01032128.
99DS-01032129.
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99DE-01032920.
99DE-01032922.
          Example, Fig 1, 35pp; English
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99DE-01032125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                 51; Conservative
                                                                                                                                                                       Similarity
                                                                                                                                        Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200100842-A2
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                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                     RESULT 14
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis
and adaptation (HA) proteins given in AAB79023 to AAB79242. The C.
glutamicum HA genes (I) can be used in vectors for expression in host
cells and production of fine chemicals, such as, an organic acid,
cells and production of fine chemicals, such as, an organic acid,
corpression or nonproteinogenic anino acid (preferred), purine or
pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
ce pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
corpression or enzyme. The amino acids produced can be lysine, glutamine,
collutamate, alanine, aspartate, glycine, serine, threonine, methionine,
corpressine, phenylalanine, or tryptophan. The fine chemical production can
complated. The presence or activity of Corynebacterium diphtheriae.
Corpressine, phenylalanine, or tryptophan. The fine chemical production can
conditated. The presence or activity of Corynebacterium diphtheriae.
Corpressine the presence or activity of Corynebacterium diphtheriae.
Corpressine conded to map the C. glutamicum genome or can be used as markers
corpressine ancoded by the (I) are used to maintain homeostasis in C.
Corpression or help the microorganism to adapt to different environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 GIRGVIVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMEIVVKKDQVESVINTILEGAR
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                                                                                                                                                                                                                                                                                                                                      Schroeder H, Zelder O, Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.9%; Score 246.5; DB 4; Length 89; 50.6%; Pred. No. 5.7e-23; ive 24; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 TGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::||||::|||| | TGKVGDGKVWMTNIBELVRVRTGERGEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 563; 712pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABBS4937 standard; protein; 112 AA
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50.6%; Fr. 24;
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                       99DE-01041378.
99DE-01041379.
99DE-01041390.
99DE-01041391.
99DE-01033006.
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                                                                                                                                                                                                                                                                                                                                          Pompejus M, Kroeger B,
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                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-061974/07.
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Best Local Similarity
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sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and patent WO20017334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at the wipo.in:/pub/published_pot_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                               The present invention is related to a Lactococcus lactis nucleotide
                                                                                                                                                                                                             New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                    Bolotine A, Sorokine A, Renault P, Ehrlich SD;
                                                                                                                                                                                                                                                                      Claim 6; SEQ ID NO 1639; 2504pp; French.
                                                                                             (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                11-APR-2000; 2000FR-00004630.
                                                         11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                    lactis and related species.
                                                                                                                                                                         WPI; 2002-043418/06.
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                                                                     3 KVEALVRPWRIQQVSSALLKIG-IRGVTVSDVRGFGAQGGSTERHGGSEPSEDKFVAKVK 61
                                                                                            2; Gaps
                                                                                                                                                               62 MEIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
 DB 5; Length 112;
                                 36; Indels
Ouery Match
40.1%; Score 225; DB 5.
Best Local Similarity 43.2%; Pred. No. 4e-20;
Matches 48; Conservative 25; Mismatches
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Sequence 112 AA;

Search completed: May 24, 2004, 19:13:02 Job time : 53 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

May 24, 2004, 19:10:08; Search time 14 Seconds (without alignments) 776.403 Million cell updates/sec Run on:

Title: Perfect score:

US-09-756-541-1 561 1 FYXVBAIVRPWRIQQVSSAL......VLPVSDVIRVRTGERGEKAE 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: piri:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description		P II nitrogen sens	nitrogen regulator									~~	nitrogen regulator				nitrogen regulator								nitrogen regulator					
	ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	D85024	F70310	AH2095	H81961	B81019	A39696	D82102	S13078	RGECP2	S04377	C91056	AF0354	AH0826	C64307	G85900	S73175	S52328	S33180	G64467	AB2794	A97573	F64062	AD3374	C87493	G70747	B82302	T35668	D69188	B69468
	DB	-	7	ď	7	N	7	Ų	Ŋ	7	П	Ċ	7	7	2	7	7	7	Ŋ	~	C4	~	7	7	ď	N	N	7	7	~	7
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ę	Query	1 1 1 1	100.0	58.4	56.8	55.0	54.8	54.6	51.6	51.2	50.7	50.7	50.7	50.7	50.7	50.4	50.2	49.8		49.3	49.3	49.1	49.1	•	48.9	48.8	48.6		46.8	46.6	46.4
	Score	1 1 1 1 1	261	,	318.5	•		306.5	289.5	287.5			284.5	284.5	284.5	282.5	281.5	279.5	276.5	276.5	276.5	275.5	275.5	274.5	274.5				262.5	ei.	260.5
	Result No.		Т	7	m	4	വ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

nitrogen regulator	glnK protein (AJ00	nitrogen regulator	nitrogen regulator	nitrogen regulator	nitrogen regulator										
AB0560	D82985	AG0381	B26567	B64775	H90691	D85542	A33600	H82631	B69188	AD2915	G97689	S76404	D87415	H87313	G86823
N	C1	~	N	N	N	N	N	N	N	۲3	N	~	N	N	7
112	112	112	111	112	112	112	111	112	115	116	116	82	112	114	113
46.3	45.9	45.9	45.8	45.7	45.7	45.7	45.6	45.5	44.8	44.7	44.7	43.8	43.6	42.5	40.1
259.5 46.3			257 45.8	256.5 45.7							250.5 44.7			238.5 42.5	

# ALIGNMENTS

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The Cold Sprin
P II nitrogen sensing protein GLB I [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Accession: D85024
R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col Nature 402, 769-777, 1999
A.Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:NC_01268; NID:g7268574; PIDN:CAB80683.1; GSPDB:GN00140 C;Genetics: A;Gene: Arag01900 A;Map position: 4
                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
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ô Gaps ·, Length 196; 0; Indels 100.0%; Score 561; DB 2; nilarity 100.0%; Pred. No. 6.8e-48; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 113; Conserv

74 FYKVEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKV 133 1 FYKVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKV ò d

9

61 KMELVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKAE 113 134 XMEIVVKKDQVESVINTIIEGARTGEIGDGKIFV1,PVSDVIRVRTGERGEKAE 186 Š g

#### RESULT 2 F70310

nitrogen regulatory protein P-II - Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: OB-May-1998 #sequence\_revision 08-May-1998 #text\_change 26-Aug-1999 C;Accession: F70310 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70310
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A;Residues: 1-112 <AQF> A;Cross-references: GB:AE000674; NID:g2982850; PIDN:AAC06473.1; PID:g2982852; GB:AE00065 A;Experimental source: strain VF5

C;Genetics: A;Gene: glnB C;Superfamily: regulatory protein P-II

Indels

58.4%; Score 327.5; DB 2; ilarity 54.5%; Pred. No. 3.5e-25; Conservative 30; Mismatches 19;

Local Similarity nes 60; Conserv

Matches

à ВÞ

dd

Query Match

C,Keywords: phosphoprotein; signal transduction F;51/Binding site: UMP (Tyr) (covalent) #status predicted

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A; Residues: 1-112 <TSI>
A; Residues: 1-112 <TSI>
A; Cross-references: G8:M62447; NID:g154517; PIDN:AAA27312.1; PID:g552028
A; A; Cross-references: PCC 7942
A; Note: the authors translated the codon CCT for residue 83 as Thr
A; Note: the authors translated the codon CCT for residue 83 as Thr
Bichii, N: Warren: P.V.; G00-bcck, J.H.; Frank, G.; Zuber, H.; Bryant, D.A.
Bichiim. Biophys. Acta 1059, 215-225, 1991
A; Title: Polypeptide composition of the Photosystem I core
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4-4
                                                                                                                                                                                                                                    3 KIEAIVKPFKLDDVREALTEIGITGMTVSEVKGFGRQKGHTEIYRGAEYAVD-FLPKVYI 61
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                                                                                                      Gaps
                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                  63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                 63 ELVVKKDQVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
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         Length 112;
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C;Keywords: phosphoprotein
F;S1/Binding site: UMP (Tyr) (covalent) #status predicted
55.0%; Score 308.5; DB 2;
55.5%; Pred. No. 2.6e-23;
ive 24; Mismatches 24;
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llarity 54.5%; Pred. No. 3.2e-23;
Conservative 25; Mismatches 24;
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                                          1 Similarity 55.5% 61; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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    Query Match
Best Local S:
Matches 61
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2010
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83744.1; PID:g737919
A.Experimental source: serogroup A, strain 22491
C.Genetics:
A.Genetics:
C.Genetics:

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C; Species: Neisseria meningitidis
C; Species: Os-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: H81951
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 532-550, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitrogen regulatory protein P-II glnB [imported] - Nostoc sp. (strain PCC 7120) C.Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AH2095
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A;Molecule type: DNA
A;Residues: 1-12 < KUR>
A;Coss-references: GR:BA000019; PIDN:BAB74018.1; PID:g17131411; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                        3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVYM
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Indels

56.8%; Score 318.5; DB 2 clarity 57.3%; Pred. No. 2.7e-24; Conservative 24; Mismatches 22

Query Match Best Local Similarity Matches 63; Conserv

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A;Residues: 1-112 <PAR> A, Accession: H81961 A, Status: preliminary A, Molecule type: DNA

HB1961

A,Gene: glnB C,Superfamily: regulatory protein P-II

C; Genetics:

A; Accession: AH2095

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A;Variety: PCC 7942; PCC 6301
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 26-Aug-1999
C;Accession: A39696; F56817
R;Tsinoremas, N.F.; Castets, A.M.; Harrison, M.A.; Allen, J.F.; Tandeau de Marsac, N. R;Tsinoremas, N.S.A. 88, 4565-4559; 1991
A;Title: Photosynthetic electron transport controls nitrogen assimilation in cyanobacter A;Reference number: A39696; MUID:91271233; PMID:1905010
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A;Experimental source: serogroup B, strain MC58
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A;Residues: 1-18, R', 20-80, B', 83-102, VVP' <SON>
A;Residues: 1-18, R', 20-80, B', 83-102, VVP' <SON>
A;Cross-references: GB:MI6778; NID:g146165; PIDN:AAA23883.1; PID:g146166
B;van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, D.
Mol. Microbiol. 9, 443-457, 1993
A;Title: The genes of the glutamine synthetase adenylylation cascade are not regulated b.
A;Reference number: S36254; MUID:94018640; PMID:8412694
                               Mol. Gen. Genet. 224, 421-430, 1990
A:Title: Characterization of three different nitrogen-regulated promoter regions for the
A:Reference number: S13078; MUID:91094780; PMID:1762507
                                                                                                                                                                                                                                                                                                                                                                                          A, Description: P-II protein synthesis is increased under conditions of nitrogen fixation C, Superfamily: regulatory protein P-II
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A;Note: sequence extracted from NCBI backbone (NCBIN:139878, NCBIP:139882)
A;Note: sequence extracted from NCBI backbone (NCBIN:139878, NCBIP:139882)
My audicant, S.G.; Armarego, W.L.F.; Shaw, D.C.; Lilley, P.E.; Dixon, N.E.; Poole, R.K. Mol. Gen. Genet. 226, 49-58, 1991
A;Title: Isolation and nucleotide sequence of the hmp gene that encodes a haemoglobin-li A;Reference number: S15991; MUID:91238719; PMID:2034230
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C;Species: Escherichia coli
C;Date: 30-Jun-1986 #sequence_revision 10-Nov-1995 #text_change 01-Mar-2002
C;Accession: C49940; S15991; A29307; S37753; H65032; S31961
R;Liu, J.; Magasanik, B.
J. Bacteriol. 175, 7441-7449, 1993
A;Title: The glub region of the Escherichia coli chromosome.
A;Reference number: A49940; MUID:94042920; PMID:8226691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                              A;Cross-references: EMBL:X51499; NID:g38664; PIDN:CAA35867.1; PID:g38665
A;Experimental source: strain SP7
C;Genetics:
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A;Cross-references: GB:X58872; NID:941730; PIDN:CAA41683.1; PID:941732
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                                                                                                                                                                                                                                                                                                                                                                                                                         C,Superfamily: regulatory process. . . . C,Keywords: phosphoprotein; signal transduction F;51/Binding site: UMP (Tyr) (covalent) #status predicted
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A;Title: Cascade control of Escherichia coli glutamine sA;Reference number: A29307; MUID:87250488; PMID:2885322
A;Accession: A29307
      Ride Zamaroczy, M.; Delorme, F.; Elmerich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain K-12
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Matches 54; Conser
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A;Molecule type: DNA
A;Residues: 1-112 <LIU>
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A;Residues: 1-12 <VAN>
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                                                                                                                                                                                                                                                                                               A, Note: modification state depends on the nitrogen source and the spectral light quality
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riffeldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A,Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A,Reference number: A82035; MUID:20406833; PMID:10952301
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C;Species: Azospirillum brasilense
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KVEAIVRPWAIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKOM
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                                                                                                                                                                                                                                                                                                                        C,Superfamily: regulatory protein P-II
C,Keywords: phosphoprotein; signal transduction
F;49/Binding site: phosphate (Ser) (covalent) #status predicted
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.6%; Score 306.5; DB 2; Length 55.5%; Pred. No. 4e-23; Lindels 1ive 23; Mismatches 25; Indels
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C,Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;S3/Binding site: UMP (Tyr) (covalent) #status predicted
A; Reference number: A56817; MUID: 91355213; PMID: 1653017
                                                                                                                                                                                                                                                                   A; Description: involved in signal transdution
                                                                                                                                            A; Experimental source: PCC 6301
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Matches 57; Conservative
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                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <LII>
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A;Status: preliminary
A;Molecule type: DNA
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A;Gene: VC2239
                                                                                                                                                                        C,Genetics:
A,Gene: gln3
C,Function:
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                               A; Accession:
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Matches
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A;Residues: 1-112 <BLAT>

A; Molecule type:

;Gene: glnB
;Function: <GEN>

<NTRB>

Function:

1;

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hypothetical protein EC83419 [imported] - Escherichia coli (strain 0157:H7, substrain R. G.Species: Escherichia coli (5.Species: Escherichia coli (5.Species: Escherichia coli (5.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C.Accession: C91056 Askino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 Askinore sequence of enterohemorrhagic Escherichia coli 0157:H7 and gence hatter and momber: A99629; MUID:21156231; PMID:11258796
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Accession: AF0354
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, W.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                      1; Gaps
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                                                                                      Indels
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                  50.9%; Pred. No. 5.9e-21; ive 27; Mismatches 26;
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C,Superfamily: regulatory protein P-II
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Les 56; Conservative
                                                                                      56; Conservative
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                  Similarity
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A;Molecule type: DNA
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                        Best Local
Matches 5
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Pathway: nitrogen regulation pathway
A;Note: this protein participates indirectly in activation of glutamine synthase activit
A;Note: under nitrogen-limiting conditions it is covalently uridylylated; in nitrogen extransferase / uridylyl-removing enzyme which is regulated by the glutamine/alpha-ketoglu
                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: de-uridylylated P-II forms a complex with nitrogen regulation protein II the uridylylated form of P-II does not complex with ntrB; free ntrB phosphorylates nitro A;Note: phosphorylated nitrogen regulation protein I (ntrC) activates transcription of C;Function: <ARR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000341; GB:U00096; NID:g1788899; PIDN:AAC75606.1; PID:g1788904;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Description: uridylylated P-II forms a complex with adenylyltransferase, this complex ylyltransferase deadenylylates glutamine synthase Avote: Eree glutamine synthase is active, adenylylated glutamine synthase is inactive C;Superfamily: regulatory protein P-II C;Reywords: phosphoprotein, signal transduction F;51/Binding site: UMP (Tyr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: important for the control of glutamine synthase; in nitrogen-limiting conto form P-II-UMP; P-II-UMP allows the deadenylation of glutamine synthetase, thus activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S04377
R;Holtel, A.; Merrick, M. 1988
Mol. Gen. Genet. 215, 134-138, 1988
A;Title: Identification of the Klebsiella pneumoniae glnB gene: mucleotide sequence of
A;Reference number: S04376; MUID:89201233; PMID:2907369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: P-II indirectly controls the transcription of the GS gene (glnA) by preventing
                                                              A Experimental source: strain K-12, substrain W3110
R Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Petna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65032
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C;Species: Klebsiella pneumoniae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: | :: | : : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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A; Cross-references: EMBL: Z21843; NID: 949395; PIDN: CAA79890.1; PID: 949397
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A;Residues: 1-112 <HOL>
A;Cross-references: EMBL:X14012; NID:g43804; PIDN:CAA32177.1; PID:g43806
A;Experimental source: strain M5a1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown
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C,Keywords: phosphoprotein; signal transduction
F,51/Binding site: UMP (Tyr) (covalent) #status predicted
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50.7%; Score 284.5; DB 1 50.9%; Pred. No. 5.9e-21; ative 27; Mismatches 26

Query Match Best Local Similarity 50.9%. Matches 56; Conservative

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à 셤 50.7%; Score 284.5;

ted, these events are reversed

A;Gene: glnB C;Function:

Genetics:

A;Accession: S04377

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Expothetical protein glnB [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;)Species: Escherichia coli (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85900 E;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005174; NID:g12516963; PIDN:AAG57667.1; GSPDB:GN00145; UWGP:Z38
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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      3 KVEAIIRPEKLEIVKKALSDAGYVGMTVSEVKGRGVQGGIVERYRGREYIVD-LIPKVKI 61
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85900
                                                                                                      63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
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50.9%; Pred. No. 1.2e-20;
ive 26; Mismatches 27;
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te : 15 secs
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C,Superfamily: regulatory protein P-II
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Best Local Similarity 50.99
Matches 56; Conservative
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A; Molecule type: DNA
A; Residues: 1-112 <STO>
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                                                                                                                                                                                                                                                                              nitrogen regulatory protein p-II STY2808 [imported] - Salmonella enterica subsp. enterid
                                                                                                                                                                                                                                                                                                 C; Species: Salmoncella enterica subsp. enterica servour Typhi
A; Note: this species has also been called Salmonchla typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AH7826
B; Parkhill, J: Dougan, G:; James, K.D; Thomson, N.R; Pickard, D.; Wain, J.; Churcher, F.; Connertor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O; Gaora, P.
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atthors: Parry, C.; Quail, M.; Rutherford, P.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servo A; Reference number: A80502; MUID: 21534947; PMID: 11677608
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         61
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3 KIDALIKPFKLDDVREALAEVGITGMTVTEVKGFGRQKGHTELYRGAEYMVD-FLPKVKI
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                                                             63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
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EIVVADDIVDTCVBAIMQTAHTGKIGDGKIFVFDVSRVVRIRTGEQDEEA 111
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Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, (A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi: A;Reference number: A64300; MUID:96337999; PMID:8688087

probable nitrogen regulatory protein P-II - Methanococcus jannaschii C:Species: Methanococcus jannaschii C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000 C;Accession: C64307

RESULT 14

50.7%; Score 284.5; DB 2; 50.9%; Pred. No. 5.9e-21;

C; Superfamily: regulatory protein P-II

STY2808

A;Residues: 1-112 <PAR>

A;Accession: AH0826 A;Status: preliminary A;Molecule type: DNA

26;

27; Mismatches

Conservative

Local Similarity

Query Match Best Local Si Matches 56;

56;

g δ

8

A,Cross-references: GB:U67464; GB:L77117; NID:q1590852; PIDN:AAB98041.1; PID:q1592259;

A;Accession: C64307 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

ij

DB 2; Length 112;

ch 50.4%; Score 282.5; DB 2; Length 1 Similarity 53.6%; Pred. No. 9.2e-21; 59; Conservative 21; Mismatches 29; Indels

Query Match Best Local S Matches 59

C;Superfamily: regulatory protein P-II C;Keywords: phosphoprotein; signal transduction F;51/Binding site: UMP (Tyr) (covalent) #status predicted

A.Map position: FOR58979-59317

A; Residues: 1-112 <BUL>

3 KVEAIVRPWRIOQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSBFSEDKFVAKVXM

1

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 24, 2004, 19:06:17; Search time 10.5 Seconds (without alignments) 560.374 Million cell updates/sec Run on:

Title: Perfect score:

US-09-756-541-1 561 1 FYKVBAIVRPWRIQQVSSAL.....VLPVSDVIRVRTGERGEKAE 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	DI	GLNB AQUAE	GLNB FREDI	GLNB NOSPU	GLNB SYNP7	GLINB SYNY3	GLNB PASMU	GLNB AZOBR	GLNB_ECOLI	GLINB KLEOX	Y059 METUR	GLNB PORPU	GLINB RHORU	GLNB_RHOSH	YD44 METJA	GLNB RHIME	GLNB HAEIN	GLNB MYCTU	GLAB RHILO	GLINB BRAJA	GLINB RHOCA	GLN2 METTH	GLNB RHILV	GLNK_ECOLI	GLNB CYACA	GLN1 METTH	GLNB RHIET	NRGB BACSU	GLN2 METBA		GLN4 METBA	GLN2 METIV	GLN2_METMP	GLN2_METTM
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GLM1 METTL GLM1 METTM GLM1 METTW GLM1 METTW GLM1 METRIV GLM1 METRIV GLM3 METRIV GLM3 METRIV SLM6 YEAST SYA HALM1 SELÜ METKA MMIL METKA MMIL METKA RS1 ENTCK RS3 EIFLO
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## ALIGNMENTS

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63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=63737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as a long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAUGHANG FACHER M.A.

Liotenherg S., Cartets A.M., Campbell D., Houmard J.,

Tandeau de Marsac N.;

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: P-11 INDIRECTLY CONTROLS TEE TRANSCRIPTION OF THE GS

-!- FUNCTION: P-11 INDIRECTLY CONTROLS TEE TRANSCRIPTION OF THE GS

NR-1-PHOSPHATE. THE TRANSCRIPTIONAL ACTIVATOR OF GINA. WHEN P-11

IS PHOSPHOYLAMED. THESE EVENTS ARE REVERSED (BY SIMILARITY).

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN

TO 2-KETOGLUTARATE DECREASES, P-11 IS PHOSPHORYLATED WHICH ALLOWS

THE DEADRAPLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
                                                                                                                                                3 KVEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKW
                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fremyella diplosiphon (Calothrix PCC 7631).
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
                                                                                                  ä
                                                                                                                                                                                                                                             SIVVKKDQVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
                                                                                                                                                                                                                                                                      58.4%; Score 327.5; DB 1; Length 112; 54.5%; Pred. No. 2.5e-26; Live 30; Mismatches 19; Indels 1;
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PROSITE; PS00456; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Mitrogen fixation; Phosphorylation.
MOD RES 49 49 PHOSPHORYLATION (PROBABLE).
SEQUENCE 112 AA, 12478 MM; F74E54C393C4596B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length
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  12497 MW; 0E44B4B171A6233B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the P(II) protein family.
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56.4%; Pred. No. 2.6e-25;
tive 25; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA
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InterPro; IPR002332; PII GlnB_UMP_S.
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     Ä
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Les 60; Conserv
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nes 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1197;
     112
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-AICC 29133 / PCC 73102;

MEDLINE-98304077; PubMed=963924;

MEDLINE-98304077; PubMed=961924;

MEDLINE-98304077; PubMed=961924;

MEDLINE-98304077; PubMed=961924;

MEDLINE-98304077; PubMed=961924;

MEDLINE-98304077; PubMed=96108 product of Nostco punctiforme or the punct
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PIM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL LIGHT QUALITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
62 EIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVVRIRTGEKNTEA 111
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PRINTS; PR00440; PIIGINB.
PRODOM; PR001194; PII glnB; 1.
PROSITE: PS006496; PII GLNB UMP; 1.
PROSITE: PS00639; PII GLNB CTER: 1.
Transcription regulation; Nitrogen fixation; Phosphorylation.
Transcription 49
PHOSPHORYLATION (PROBABLE).
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InterPro, IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
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us-09-756-541-1.rsp

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GLNB SYNY3
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J. Bacteriol. 177:5912-5917(1995).
-!-FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
IS PHOSPHATE, THE TRANSCRIPTIONS ARE REVERSED.
-!-FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLONS
THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
THE ENZYME.
                                                                                                                                                                                                                                                                                       "Photosynthetic electron transport controls nitrogen assimilation in cyanobacteria by means of posttranslational modification of the glnB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrison M.A., Keen J.N., Findlay J.B.C., Allen J.F.; "Modification of a glnB-like gene product by photosynthetic electron transport in the cyanobacterium Synechococcus 6301."; FBSS Lett. 264:25-28(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94110245; PubMed=8282715;
Forchhammer K., Tandeau de Marsac N.;
Forchimmer T. Tandeau de Marsac N.;
"The PII protein in the Cyanobacterium Synechococcus sp. strain PCC
7942 is modified by serine phosphorylation and signals the cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bryant D.A.;
                                                         01-MAY-1991 (Rel. 18, Created)
U-MAY-1992 (Rel. 22, Last sequence update)
28-FKB-2003 (Rel. 41, Last amocation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                 Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2), and Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETRAIN-ECC 6301;
MEDLINE-91355213; PubMed=1653017;
Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., Bryant D "Polypeptide composition of the Photosystem I complex and the Photosystem I core protein from Symechococcus sp. PCC 6301."; Biochim. Biophys. Acta 1059:215-225(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forchhammer K., Tardeau de Marsac N.;
"Phosphorylation of the PII protein (glnB gene product) in the
cyanobacterium Synechococcus sp. strain PCC 7942: analysis of
                                                                                                                                                                                                                         STRAIN=PCC 7942;
MEDLINE=91271233; PubMed=1905010;
Tsinoremas N.F., Castets A.M., Harrison M.A., Allen J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                               "Genes required for c-type cytochrome biogenesis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      gene product.";
Proc. Natl. Acad. Sci. U.S.A. 88:4565-4569(1991)
                              112 AA
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90249505; PubMed=2110911;
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MEDLINE=96011366; PubMed=7592328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 176:84-91(1994)
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Homotrimer,
                                                                                                                                                                                                                                                                                                                                                                                                 Inoue K., Bryant D.A.;
                                                                                                                                                                               NCBI TaxID=1140, 1139
                                                                                                                                                                                                                                                                         Pandeau de Marsac N.;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PCC 6301;
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=PCC 6301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION.
                                         P800<u>1</u>6;
01-MAY-1991
                            GLNB SYNP7
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           SYNP7
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PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL

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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsumo A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 [1996]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
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PROSITE; PS00496; PII_GLNB UMP; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
Transcription regulation; Mitrogen fixation; Phosphorylation.
MOD_RES 49 PHOSPHORYLATION.
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    -!- SIMILARITY: Belongs to the P(II) protein family.

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T -> P (IN REF. 1;
5F44B64CBFF3C5S9
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56.4%; Pred. No. 8.2e-25;
tive 23; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP S.
Pfam; PF00543; P-II; 1.
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Plant Mol. Biol. 35:723-734(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF079137; AAF04333.1; -. PIR; A39696; A39696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M62447; AAA27312.1;
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PhosSite; P80016; -
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HSSP; P05826; 2PII
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ID GLNB AZOBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotrimer (By similarity).
PTM: PHOSEPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL
EUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLAA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
KEL-I-PHOSPHATE. THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY).
FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GINA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GINA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Nitrogen fixation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F9ABD0F5C173B799 CRC64;
                                                                                                                                           LIGHT QUALITY (BY SIMILARITY). SIMILARITY: Selongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.7%; Score 312.5; DB 1
54.5%; Pred. No. 8.2e-25;
iive 26; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                         entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
                                                                                                                                                                                                                                                                                                EMBL; X97496; CAA66127.1; -.
EMBL; D90915; BAA18533.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_
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GLNB OR PM2004.
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Matches 60; Conservative
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PRINTS; PR00340; PIIGLNB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella multocida.
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MOD RES 49
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Q9CJK1;
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                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement [See http://www.isb-sib.ch/anrounce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KWEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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Biochimie 68:1181-1187(1986).
-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLA
EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE
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"Nucleotide sequence of the Azospirillum brasilense Sp7 glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Zamaroczy M., Delorme F., Elmerich C.;
"Characterization of three different nitrogen-regulated promoter regions for the expression of glnB and glnA in Azospirillum brasilense.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Witrogen fixation; Complete proteome.
BINDING 51 51 UMP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 BIVVTDEQVDQCIEAIMETAQTGKIGDGKIFVYDVBRVIRIRTGEBNBDA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 112;
                                                                                                                   SUBUNIT: Homocrimer (By similarity).

PIM: Uridylylated/deuridylylated by glnD (By similarity).

SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCC9D24651F47642 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%; Score 290.5; DB 1
53.6%; Pred. No. 1,4e-22;
ive 21; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR002187; PII glnB.
InterPro: IPR002332; PII GlnB UMP S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERMITS PRO0543; P-II; 1. PRINTS; PRO0340; PIIGLNB.
PRODON; PD001194; PII glnB, 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Gen. Genet. 224:421-430(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87076765; PubMed=2878685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91094780; PubMed=1702507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrogen regulatory protein P-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006236; AAK04088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 112 AA; 12684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 88-112 FROM N.A.
                                                                                          ENZYME (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azospirillum brasilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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us-09-756-541-1.rsp

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HIA BERKER KERKER KAN KERKER K
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or serd an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Son H.S., Rhee S.G., "Cascade control of Escherichia coli glutamine synthetase. Purification and properties of PII protein and nucleotide sequence of
             P-11-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHERAGE (68), THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-11 IS DEURIDYLATED AND PROMOTES THE ADENTATION OF GS.
FUNCTION: P-11 INDIRECTLY CONTECLS THE TRANSCRIPTION OF THE GS GENE (GLNA). P-11 PREVENTS NR-11 CATALYZED CONVERSION OF NR-1 TO NR-1-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-11 IS URITYLYLATED TO P-11-UMP, THESE EVENTS ARE REVERSED.
SUBUNIT: HOMOTIMER (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrogen regulatory protein P-II 1.
GLNB OR B2553 OR C3076 OR 23829 OR ECS3419 OR STM2561 OR STY2808 OR
  TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 EIVVKKOOVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 51.2%; Score 287.5; DB 1; Length 1 Similarity 49.1%; Pred. No. 2.8e-22; 54; Conservative 27; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B6258EC9C4B63871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00543; F-11, 1.

PRINTS; PR00340; PIGLARB.

PRODOR; PS00496; PII GLNB LMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Transcription regulation; Nitrogen fixation.

51 UMP.
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01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562, 217992, 83334, 602, 601, 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; MZ6107; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, POS826; 2PII.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB.UMP-
Pfam; PP00543; P-II, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=E.coli;
MEDLINE=87250488; PubMed=2885322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 112 AA; 12371 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51499; CAA35867.1; -.
EMBL; M26107; -; NOT ANNOTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli C6,
Escherichia coli C157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T0295 OR SF2600 OR S2772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium,
Salmonella typhi, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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SPECIES=E.coli; STRAIN=K12;
MEDLINE=97499980; PubMed=9205837;
MEDLINE=97499980; PubMed=9205837;
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satch Y., Sivasurnâram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C.,
Yamaqata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"R.2 genome corresponding to 50.0-68.8 min on the linkage map and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.

SPECIES=B.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIESEE.coli; STRAIN=K12;
MEDLINE=91238719; PubMed=2034230;
Vasudevan S.G., Armarego W.L.F., Shaw D.C., Lilley P.E., Dixon N.E., Poole R.K.;
"Isolation and nucleotide sequence of the hmp gene that encodes a haemoglobin-like protein in Escherichia coli K-12.";
Mol. Gen. Genet. 226:49-58(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SECIES=E.coli; STRAIN=KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Gregor J., Shao Y.;
                                                                                                                                                                                                                            Holtel A., Merrick M.;
"Identification of the Klebsiella pneumoniae glnB gene: nucleotide
sequence of wild-type and mutant alleles.";
Mol. Gen. Genet. 215:134-138(1988).
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck F.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       igasanik B.;
region of the Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
s structural gene.";
Biol. Chem. 262:8690-8695(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli;
MEDLINE=94042920; PubMed=8226691;
Liu J., Magasanik B.;
"The glnB region of the Escherich:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of uropathogenic Escherichia coli.
                                                                                                                                                                                    MEDLINE=89201233; PubMed=2907369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 175:7441-7449 (1993)
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                                                                    [2]
REVISIONS TO C-TERMINUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEÇUENCE FROM N.A.
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Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella
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01-0CT-1989 (Rel. 12, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                         flexneri Berotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95171116; PubMed=7866749;
                                                                                                                                                                                   SPECIES=E.coli;
MEDLINE=90089474; PubMed=2574599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89201233; PubMed=2907369;
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                                                                                                                                                                                                                                                                                                                                                                  CRYSTALLIZATION, AND SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligomeric structure.";
FEBS Lett. 337:255-258(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=E.coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=571;
                                                                                                                                                                                                                                       Magasanik B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=M5a1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLINB KLEOX
                                                                                                                                                           REVIEW
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GENB_KLEOX
  RAH KATAKA KATAKAKA KATAKA KATAKA KATAKA KATAKA KATAKA KATAKA KATAKA KATAKA KATAKAKA KATAKA K
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SPECIES=E.coli; STRAIN=c157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=1125895;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Tida T., Tasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S. Lyphi; STRAIN=Ty2 / AICC 700931; MEDLINE=22531367; PubMed=12644504; MEDLINE=22531367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyiami V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.Cyphimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21554948; PubMed=11677609;
MCCICLILARE—2154948; PubMed=11677609;
MCCICLILARE M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 [2002].
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-12 FROM N.A.
SPECIESES...Coll; STRAIN=K12 / W3110;
MEDILINE=94018640; PubMed=4412694;
van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.;
"The genes of the glutamine synthetase adenylylation cascade are not regulated by nitropen in Bscherichia coli.";
Mol. Microbiol. 9:443-45911993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.Cyphi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Eaker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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MEDLINE=22272406; PubMed=12384590;
Jin C., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding X., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
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Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
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"Regulation of transcription of the glnALG operon of Escherichia coli
by protein phosphorylation.";
Biochimie 71:1005-1012(1989).
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Structure 2:981-990(1994).
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Enterobacteriaceae; Klebsiella.
                                                                                                              SPECIES=E.col;
MEDLINE=24123764; PubMed=8293810;
Vagudevan S.G., Geder C., Dixon N.E., Cheah E., Carr P.D.,
Vagufcolk P.M., Jeffrey P.D., Ollis D.L.;
Suffolk P.M., Jeffrey P.D., Ollis D.L.;
"Recherichia coli PII protein: purification, crystallization and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%; Score 284.5; DB 1; Length 50.9%; Pred. No. 5.6e-22; Indels iive 27; Mismatches 26; Indels
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EMBL; U38804; AACO8140.1; -. PIR; S73175; S73175.
HSSP; P05826; 2PII.
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HSSP; P38504; 1GNK.
TIGR; MJ0059; -.
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GLNB_PORPU
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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STRAINS-JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Rlake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinster K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.
-!- SUBUNIT: Homotrimer (By similarity).
-!- SIMILARITY: Belongs to the P(II) protein family.
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical nitrogen regulatory PII-like protein MJ0059.
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Methanocaldococcaceae; Methanocaldococcus.
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-!- SIMILARITY: Belongs to the P(II) protein family.
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PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                              PIR; S04377; S04377.
HSSP, P058266, 2PII.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
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Bukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Plant Mol. Biol. Rep. 13:333-335 (1995).
Plant Mol. Biol. Rep. 13:333-335 (1995).
PUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETAXE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDIVIATED TO P-II-UNP. THESE ACTIVATOR OF GLNA. WHEN P-II IS URIDIVIATED TO P-II-UNP.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0340; PIIGENB.
PRODOM; PD001194; PII.glnB; 1.
PROSTTE; PS00638; PII.GLNB CTER; 1.
Hypothetical protein; Transcription regulation; Complete proteome.
BINDING 51 51 UMP (BY SIMILARITY).
SEQUENCE 112 AA; 12490 MM; 3DC3F307C32F59F3 CRC64;
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Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVVXKDQVESVINTIIBGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
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-!- SIMILARITY: Belongs to the P(II) protein family.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
institutions as long
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NCBI_TaxID=1063;
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P43519;
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                                                                                                                                                                                                                  3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-ATCC 11170 / S1;

Zhang Y., Ludden P.W., Roberts G.P.;

Zhang Y., Ludden P.W., Roberts G.P.;

Zhang Y., Ludden P.W., Roberts G.P.;

LIDIAL STRUCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLOTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR.II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DEADENDENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME.

SUBUNIT: HOMOLIMMER (By similarity).

-! SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johansson M., Nordlund S.; "Transcription of the glub and glnA genes in the photosynthetic bacterium Rhodospirillum rubrum."; Microbiology 142:1265-1272(1996).
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end
                                                                                                                                                                                                                                                      63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                      EIIVSDDXVXSITEIIIXTAXTGEIGDGKIFISDVEQVIRIRTNDLNSAA 111
                                                                                                                                              49.8%; Score 279.5; DB 1; Length llarity 51.8%; Pred. No. 1.8e-21; Conservative 21; Mismatches 31; Indels
                                                                                         Transcription regulation; Mitrogen fixation; Chloroplast.
BINDING 51 51 UMP (BY SIMILARITY).
SEQUENCE 112 AA; 12320 MM; 29416AA49FC37A18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  112 AA
InterPro; IPR002187; PIT_glnB.
InterPro; IPR002332; PIT_GlnB_UMP_S.
Pfam; PF00543; PII; 1.
PRINTS; PR00340; PIIGINB.
                                                   ProDom; PD001194; PII_GlnB; 1.
PROSITE; PS00496; PII_GLNB UMP; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 11170 / S1;
MEDLINE=96254013; PubMed=8704966;
                                                                                                                                                                                                                                                                                                                                                                                                                 Nitrogen regulatory protein P-II.
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HSSP; P05826; 2PII.
InterPro; IPR002187; PII_glnB.
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                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodospirillum rubrum
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                               Query Match
Best Local
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GLNB_RHORU
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Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;
"Nucleotide sequence and characterization of the Rhodobacter
sphaerotides glnB and glnA genes.";

Microbiology 140.2143-2151(1994).

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE
GLUTAMINE SYNTHERIASE GRNE (GLNA). P-II PREVENTS NR.-II CATALYZED
CONVERSION OF NR.-I TO NR.-I-PHOSPHATE, THE TRANSCRIPTIONAL
ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE
EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE
DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME.
-I- SUBBUNT: Homotrimer (By similarity).

-I- SUBBUNT: Belongs to the P(II) protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last amocation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                DB 1; Length 112;
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                                                                                                                                                                                                                                         MP (BY SIMILARITY).
11A3589FC97C4EBC CRC64;
                                                                                                                                                                                                                                                                                                                                         49.3%; Score 276.5; DB 1;
48.2%; Pred. No. 3.6e-21;
tive 27; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PR051TE; PS00496; PII GLNB UNP; 1.
PR051TE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation.
                                                                                                   ProDom; PD001194; PII_glnB; 1.
PROSITE; PS00496; PII_GLNB UMP; 1.
PROSITE; PS00648; PII_GLNB CTER; 1.
Transcription_regulation; Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AA
InterPro, IPR002332; PII_GlnB_UMP_S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
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InterPro, 1PR002187, PII_glnB.
InterPro, 1PR002332, PII_GlnB_UMP_
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112 AA; 12420 MW;
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarion
hes 53; Conservative
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3 KVBAIIRPEKLEIVKKALSDAGYVGWTVSEVKGRGVQGGIVERYRGREYIVD-LIPKVKI 61
                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=382;
                                                                                                                                                                                                         01-NOV-1997
01-NOV-1997
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                                                                                                                                                                     GLNB RHIME
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                                                                                                                                   3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                         3 KIEALIKPFKLDEVKEALQAAGVQSLSVTEVKGFGRQKGHTELYRGAAYVUD-FLPKVKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN JAL-1 / DSM 2661 / ATCC 43067;

MEDLINES-9637999; PubMed=8680887;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghaen N.S.M., Weidman J.R., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts R.M., Huretk M.A., Kaine B.P., Boordovsky M.,

Kienk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
Hypothetical protein; Transcription regulation; Complete proteome.
BINDING 51 mmb (pv craffice).
                                                                                                                                                                                                             63 EIVVKKOQVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
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                                                                                                                                                                                                                                                 62 EVVLADÓMVEAAVEAIVSASRIDKIGDGKIFISPVEQAIRIRIGETGEDA 111
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                                                        DB 1; Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical nitrogen regulatory PII-like protein MJ1344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                12100 MW; B278486AC9EB17D3 CRC64;
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112 AA; 12532 MW; 3DDCE2A0F32FB9F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the P(II) protein family.
(BY SIMILARITY).
                                                      49.3%; Score 276.5; DB 1 46.4%; Pred. No. 3.6e-21;
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54.2%; Pred. No. 3.6e-21;
tive 19; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                  112 AA
                                                                                            28; Mismatches
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  UMP
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                                                                                              Conservative
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Methanococcus jannaschii.
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51
112 AA;
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TIGR; MJ1344; -.
                                                                        Local Similarity
Les 51; Conserv
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                  SECUENCE
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  BINDING
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KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium melliol: grain 1021."
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
Proc. Concritor in NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GIN
TO 2-KETOGLUTARATE DECREASES, P-II IS URIDIYILATED TO P-II-UMP.
P-II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS).
THUS ACTIVATING THE BUZYME. CONVERSELLY, IN NITROGEN EXCESS P-II
S DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHAIE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLAIED TO P-II-UMP, THESE EVENTS ARE REVERSED.
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BINDING 51 51 0MP (BY SIMILARITY).
SEQUENCE 112 AA; 12281 MW; 85E6465E64B57001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=RCR2011 / SU47;
MEDLINE=970B5050; PubMed=8931324;
Arcondeguy T., Huez I., Fourment U., Kahn D.;
Symbiotic nitrogen fixation does not require adenylylation of glutamine synthetase I in Rhizobtum meliloti.";
PEMS Microbiol. Lett. 145:33-40(1996).
                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF
EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                      (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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PROSITE; PS00496; PII_GLNB UMP; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
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Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrogen regulatory protein P-II. GLNB OR R01639 OR SMC00947.
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InterPro, IPR002332; PII GlnB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00340; PIIGLNB.
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U50385; AAC44623.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00543; P-II; 1
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                                                                                                                                                                                                                                                                                                       SOLUTION SOL
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1;
Query Match
49.1%; Score 275.5; DB 1; Length 112;
Best Local Similarity 48.6%; Pred. No. 4.6e-21;
Matches 52; Conservative 27; Mismatches 27; Indels 1; Gaps
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₹ Ωp

Dp

Search completed: May 24, 2004, 19:13:34 Job time : 11.5 secs

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May 24, 2004, 19:09:38 ; Search time 36 Seconds (without alignments) 990.377 Million cell updates/sec
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561
1 FYKVEAIVRPWRIQQVSSAL.......VLPVSDVIRVRTGERGEKAE 113
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL_25:*

1: sp_archea:*
2: sp_tungi:*
3: sp_tungi:*
5: sp_invertebrate:*
6: sp_manman:*
7: sp_inc:*
8: sp_craganelle:*
9: sp_phage:*
1: sp_roganelle:*
1: sp_rodanelle:*
2: sp_virus:*
1: sp_vortebrate:*
3: sp_virus:*
3: sp_virus:*
3: sp_virus:*
3: sp_virus:*
4: sp_rodanelle:*
5: sp_virus:*
5: sp_virus:*
6: sp_virus:*
7: sp_virus:*

                                                                                                                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SS	Description	Q9zst4 arabidopsis	Q9zst5 ricinus com	Q9ari4 medicago sa	Q7v5r4 prochloroco	Q91422 anabaena sp	Q8dla5 synechococc	Q9laq3 synechococc	Q9jwc4 neisseria m	Q9jxk6 neisseria m	Q8gqs4 acetobacter	Q7vpk6 haemophilus	Q91400 prochloroco	Q7v025 prochloroco	Q7uuzl rhodopirell	Q7va51 prochloroco	Q7u8z7 synechococc
SUMMARIES	a	Q9ZST4	Q9ZST5	Q9ARI4	Q7V5R4	Q9L422	Q8DLA5	O9LAQ3	O9JWC4	Q9JXK6	Q8GQS4	Q7VPK6	Q9L400	Q7V025	07UUZ1	Q7VA51	Q7U8Z7
	DB	10	10	10	16	16	16	7	16	16	N	16	N	16	16	16	9
	Query Match Length DB	196	197	194	112	112	112	112	112	112	112	112	112	112	133	112	112
÷	Query Match	100.0	90.7	87.3	57.5	56.8	9.99	56.4	55.0	54.8	54.5	54.3	54.1	54.1	53.7	53.2	53.0
	Score	198	509	490	322.5	318.5	317.5	316.5	308.5	307.5	305.5	304.5	303.5	303.5	301.5	298.5	297.5
	Result No.	-	7	m	4	ľ	ø	7	8	0	10	11	77	13	14	15	16

Q9ezq2 azoarcus sp Q97mf6 vibrio para Q8Avi2 neisseria m Q8dbe2 vibrio vuln Q8bb5 shewanella Q9kp3 vibrio chol Q8kij5 neisseria m Q1188 rhodobacter Q8zcg9 yersinia pe Q7wj1 bordetella Q7wj1 bordetella Q7wj2 bordetella Q7wg9 bordetella Q7wg9 bordetella Q7wg9 bordetella Q9x705 corynebacte P94125 azorhizobiu Q8xd5 shewanella Q9x70 corynebactella Q9x70 corynebactella Q9x70 corynebactella Q9x70 corynebactella Q8xd5 bordetella Q8xd5 corynebacteri Q8xd5 bordetella me Q8kd5 berbaspiril Q9db2 corynebacteri Q8kd5 berbaspirilu Q9a6w4 caulobacteri Q9a6w4 caulobacteri Q9kdy10 neisseria m Q9a6w4 caulobacteri Q9kdy10 neisseria m	Q8Ki77 neisseria m
	Q8KI77
10 10 10 10 10 10 10 10 10 10 10 10 10 1	20
11.00	100
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	48.48.5
229336 229336 229336 239	271.5
11112222222222222222222222222222222222	4. 4. 4. 7.

## ALIGNMENTS

us-09-756-541-1.rspt

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SEQUENCE FROM N.A.
MEDLINE=22825698; PubMed=12917642;
                           Query Match
Best Local Similarity 90.34
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                   Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Leb J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
R. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
R. Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
R. Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
R. Shinit ALOSSOS, AACT83313.1;
R. Shill, ALOSSOS, AACT83273.1;
R. Shill, BENGSOS, AACSSOSSOS, R. Shill.
R. PIR, DBSOS4; DB
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalypheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
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MEDILE=99030678; PubMed=9811909;
MEDILE=93030678; PubMed=9811909;
"A PII-like protein in Arabidopsis: putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 561; DB 10; Length 196; 100.0%; Pred. No. 4.5e-48; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:005680B; P:regulation of nitrogen utilization; IEA.
Interpor; PR002181; PII_glnB.
PRINTS; PR00340; PII_glnB.
PRINTS; PR00340; PII_glnB.
PRODOM; PD010194; PII_glnB.
PROSITE; PS00638; PII_glnB.
PROSITE; PS00638; PII_glnB.
PROSITE; PS00638; PII_glnB.
PR00ENCE 196 AA; 21275 WW; PE740EA66776P157 CRC64;
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GO; GO:0006808; P:regulation of nitrogen utilization; IBA.
InterPro: PPR002187; PII_GINB.
PFR0543; P-II; 1.
PRINTS; PR00340; PIIGINB.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAY-1999 (TrEMBLrel. 10, Created)
MAY-1999 (TrEMBLrel. 10, Last sequence update)
JUN-2093 (TrEMBLrel. 24, Last annotation update)
protein (Fragment).
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EMBL; AR095454; AAC78332.1; -.
HSSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AA
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PROSITE; PS00638; PII GLNB CTER; 1.
NON TER
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Matches 113; Conservative
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                                                                                                                                                         72 FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV 131
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                                                                                                         1 FYKVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKV
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                                                        Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                             61 KMEIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKAE 113
                                                                                                                                                                                                                                                             184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.3%; Score 490; DB 10; Length 194; ilarity 85.0%; Pred. No. 5.5e-41; Conservative 10; Mismatches 7; Indels C
  Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0030234; F:enzyme regulator activity; IEA. GO; GO:000680B; P:regulation of nitrogen utilization; IEA
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garcia-Ibilcieta D., Sengupta-Gopalan C.;
"Characterization of PII (GLNB) in alfalfa.";
submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY027892; AAX16221.1;
HSSP; P38504; IGNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
SEQUENCE 194 AA; 21413 WW; 23FA623FF4D97450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                        7:
Score 509; DB 10;
Pred. No. 7.1e-43;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                            194 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002187; PII_glnB.
     90.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago sativa (Alfalfa).
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us-09-756-541-1.rspt

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1; Gaps

Indels

22;

24; Mismatches

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63; Conservative
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            Matches
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                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                              Gonzalez L., Phalip V., Zharg C.C.; "Phosphorylation of the signal transduction protein PII by the Ser/Thr kinase PknC in the cyanobacterium Anabaena sp. strain PCC 7120."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          1; Gaps
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P., Ablgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan W.B., Ting C.S., Tolonen A., "Gebome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
                                                                                                                                                                                                                                                                63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                              DB 16; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO: GO:0030234; F:enzyme regulator activity; IEA.
GO: GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glub.
InterPro; IPR002332; PII Glub.WMP.S.
                                                                                                                                                                                       24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                    112 AA; 12362 MW; 5CA64D6663ED3B65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AA; 12492 MW; F74E54C38B67596B CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
PII protein (Nitrogen regulatory protein P-II)
GLNB OR ALL2319
                                                                                                                                                           57.5%; Score 322.5; DB 16
58.2%; Pred. No. 1.5e-24;
tive 21; Mismatches 24.
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Pred. No. 3.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                            112 AA
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PRODOM; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                             Mature 424:1042-1047(2003).
EMBL; BX572099; CAE21656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ251822; CAB75358.1; -.
EMBL; AP003589; BAB74018.1; -.
PIR; AH2095; AH2095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.8%;
                                                                                                                                                                                      64; Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05826; 2PII.
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                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobace
NCBI_TaxID=103690;
                                                                                                                        Complete proteome.
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SEQUENCE 112 AA
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STRAIN=PCC 7120
                                                                                                                                   SEQUENCE
                                                                                                                                                              Query Match
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Best Local Similarity

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3 KVEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRHGGSEFSEDKFVAKVKW 62
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                          Gaps
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BUDINER=2225144; PubMed=12240834;

BARDINER=2225144; PubMed=12240834;

BARAMURA Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Mateumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Symechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=32049;
                                                                                           63 EIVVKKDQVBSVINTIIBGARIGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 EIVVKKDOVESVINTIIEGARIGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 EIVVEDNQVDMVVAKIIEAARTGEIGDGKIFVTPVEQVIRIRTSEKDHEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ;
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                                                                                                                      EMBL: APPOSS DE BACOSTA: 1; -. GO; GO:0030234; F:enzyme requiator activity; IEA. GO; GO:0006808; F:enzyme requiator of nitrogen utilization; IEA. InterPro; IPR002187; PII glnB. InterPro; IPR002332; PII GlnB UMP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12574 MW; 0248FDAF39505E06 CRC64;
                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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58.2%; Pred. No. 4.8e-24;
tive 22; Mismatches 23;
                                                                                                                                                                                                                                                            112 AA
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                                                                                                                                                                                                                                                                             QBDLA5;
01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00340; PIIGLNB.
PRODOM; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                      Nitrogen regulatory protein P-II
GLNB OR TLL0591.
                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 23,
                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrBMBLrel.
01-OCT-2003 (TrBMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCBI_TaxID=32046;
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SEQUENCE 112 AA
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01-OCT-2000 (
01-OCT-2000 (
01-OCT-2003 (
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oc, corp. processes, priging. Interpro; IPR002187; Priging.UMP_S. Interpro; IPR002332; Pri_Ging_UMP_S.
                                                                                                                                                                                                                                                                                                                                                      Q9JXX6;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:1809-1815(2000).
EMBL, AE002548; AAF42322.1;
PIR, BB1019; BB1019.
HSSP, PO5835; ZPII.
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les 60; Conservative
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PRINTS; PR00340; PIIGLNB.
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                                       61; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                    Similarity
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Query Match
Best Local
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Q8GQS4
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Matches
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MEDLINE-22295 / Serogroup A / James K.D., Bentley S.D., Churcher C.,
Parkhill J., Achtman M., James K.D., Bentley S.D., Chillingworth T.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis E., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
TComplete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 EIVVKKDQVESVINTIIBGARTGEIGDGKIFVLPVSDVIRVRIGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakamoto I., Gruber I., Bryant D.A.; "Nucleotide sequence of glnB and bcp genes in Synechococcus sp. PCC7002.";
                                                                                                                                                                                                                                                                                                                                                                                                                               56.4%; Score 316.5; DB 2; Length 112; 54.5%; Pred. No. 6.1e-24; ive 27; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup A).
Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mature 404:502-506(2000).

Mature 404:502-506(2000).

EMBL, AL162753; CAB83744.1; -.

EMBL, AL162753; CAB83744.1; -.

HSSP, P05826; P2FII.

GO; GO:0030234; F:enzyme regulator activity; IEA.

GO; GO:0006608; P:regulation of nitrogen utilization; IEA.

InterPro; IPR002187; PII glnB.

InterPro; IPR002183; PII glnB.

InterPro; IPR002332; PII GlnB.UMP.S.
                                                                                                                                                                                       GO. GO. 0330234; Frenzyme regulator activity; IEA. GO. GO. 0300234; Frenzyme regulator of nitrogen utilization; IEA. InterPro; IPR002187; PII_glnB. InterPro; IPR002332; PII_glnB_UMP_S.
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                                                                                                                PCC7002.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
SMBL; AF120107; AAF63031.1; --
HSSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                              PRINTS; PR00340; PIIGINB.
PROMOS PRO03194; PII GINB; 1.
PROSITE; PS00638; PII GINB CTER; 1.
PROSITE; PS00496; PII GINB UMP; 1.
SEQUENCE 112 AA; 12432 WW; C3F0AA5625E9F870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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PRINTS; PR00340; PIIGINB.
ProDom; PD001194; PII GINB. 1.
PROSITE; PS00496; PII GINB_UMP; 1.
PROSITE; PS00496; PII GINB_UMP; 1.
Complete proceome.
SEQUENCE 112 AA; 12281 MW; CD893CF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conservative
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                                                                                                                                                                                                                                                                     InterPro; IPR002332; P.
Pfam; PF00543; P-II; 1
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Best Local Similarity
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                    SEQUENCE FROM N.A.
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Q9JWC4
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                                                                                                 3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                            FIRELINE 2015755; PubMed=10710307;

MEDLINE=2015755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Bisen J.A., Ketchum K.A., Hood D.W., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Haft D.H., Salzberg S.L., White O., Pleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Mann T., Ciecko A., Markganni W., Plizza M., Grandi G., Sun L.,

Gill J., Scarlato V., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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                                                   Gaps
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Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.8%; Score 307.5; DB 16; Length
54.5%; Pred. No. 4.8e-23;
ive 25; Mismatches 24; Indele
55.0%; Score 308.5; DB 16; Length
55.5%; Pred. No. 3.8e-23;
.ive 24; Mismatches 24; Indels
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SEQUENCE 112 AA; 12311 MW; 22963CF2526D4332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Nitrogen regulatory protein P-II.
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58; Conservative
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                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=strain PCC 9511;
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                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=100363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=59919;
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                                                                                                                                                                                                                              GlnB protein.
         62
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                                                                                                                                           Q9L400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q77025
                                                                                                                      Q9L400
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                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                      Acetobacter diazotrophicus (Gluconacetobacter diazotrophicus).
Bacteria; Protecbacteria; Alphaprotecbacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 BIVCADNLVDRAVETIMAAARTGRIGDGKIFILPVEDVIRIRTGEHGEEA 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 304.5; DB 16; Length 112; 53.6%; Pred. No. 9.6e-23; arive 25; Mismatches 25; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus ducreyi.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                              GO; GO:0030234; F:enzyme regulator activity, IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_GlnB.
InterPro; IPR00332; PII_GlnB_UMP_S.
Pfam; PP00543; P-II; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur I Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducrey!";
submitted (JUN-2003) to the EMBL/Genbank/DDBJ databases.
EMBL; AR017151; AAP95074.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IndelB
                                                                                                                                                                                                                                                                                  Perlova O., Meletzus D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318039; AAN59757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Printis, PROD340; Pijans.
PRODOM; PRO01194; PII glnB; 1.
PROSTIE; PSO0638; PII GLNB CTER; 1.
PROSTIE; PSO0496; PII GLNB UMP; 1.
SEQUENCE 112 AA; 12431 NW; 52AB6F9COCC8D124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA; 12570 MW; 9977658EA4864C90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
putative nitrogen regulatory protein P-II.
                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 54.5%; Score 305.5; DB 2; Similarity 52.7%; Pred. No. 7.6e-23; 58; Conservative 25; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                            Regulatory protein PII GLNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 59; Conserv
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Matches 58; Conserv
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SEQUENCE 112 AA;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=33896;
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                                                                                                                                                                                                                                                                    STRAIN=PAL5;
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3 KVEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
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Rippka R., Tandeau de Marsac N.;

"In spite of synthesizing a cyanobacterial-type PII protein, the cocamic photosynthetic prokaryote Prochlorococcus marinus, strain PCC 9511, is unable to utilize nitrate.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, Al271089; CAB87556.1;

HSSP, P38504; IGNK.
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahigren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Shapren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb B.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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EVVVENEKVSSVIDAIAEAAKTGEIGDGKIFISSIDSVVRIRTGDTDEEA 111
54.1%; Score 303.5; DB 2; Length 112; 52.7%; Pred. No. 1.2e-22; ive 27; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Prochlorococcus sp. (strain PCC 9511).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO: GO:0030234; F:enzyme regulator activity; IEA.
GO: GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro: IPR002187; PII_glnB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF00543; P-II; 1.
PRINTS; PR00340; PIIGIAB.
ProDom; PD001194; PII glnB; 1.
PROSITE; P00638; PII GINB CTER; 1.
SEQUENCE 112 AA; 12314 MW; 42B3497E6B4472CD CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II.
                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                     3 KVBAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                     3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.7%; Score 301.5; DB 16; Length 133; 54.5%; Pred. No. 2.4e-22; Indels 1; ive 27; Mismatches 22; Indels 1;
                                                                   DB 16; Length 112;
                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Nitrogen requiatory protein P-II.
GLNB OR RE2975.
Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Planctomycetales; NCBI_TaxID=117;
                                                                54.1%; Score 303.5; DB 16; Length
52.7%; Pred. No. 1.2e-22;
tive 27; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA; 14941 MW; 05D489DB4D7B169D CRC64;
                                     112 AA; 12314 MW; 42B3497E6B4472CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL; BX294138; CAD72936.1; -.
Complete proteomer.
SEQUENCE 133 AA; 14941 MW; 05D489DB4D7B169D CI
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                                                                                                                                                                                                                                                                              133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
Nature 424:1042-1047(2003).
EMBL; BX57204; CAE19922.1; -.
Complete proteome.
SEQUENCE 112 A., 12314 MW;
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Matches 60; Conservative
                                                                               Local Similarity 52.7% nes 58; Conservative
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;

SEQUENCE FROM N.A.

Prochlorococcus. NCBI\_TaxID=1219;

u.-UCT-2003 (TEMBLEEL 25, Last sequence update)
Nitrogen regulatory protein PII.
Prochleen

Q7VA51;

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3 KVBAIVREWRIQOVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486;
Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Rakarova K.S., Ostrowski M., Oztass S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess M.R.;
Welf Y.I., Hess M.R.;
Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphotocrophic genome.", Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
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                                                                                                                                                                                                                                                                                                            53.2%; Score 298.5; DB 16; Length 112; 52.7%; Pred. No. 3.8e-22; Live 24; Mismatches 27; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           58; Conservative
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Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 24, 2004, 19:05:42 ; Search time 51 Seconds	(without alignments)	626.037 Million cell updates/sec
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US-09-756-541-2 557 Title: Perfect

1 FYKVEAILRPWRVSQVSSAL......LLPWSDVIRVRTGERGDKAE 113 score:

Scoring table: Sequence:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:  $\mathring{\boldsymbol{\beta}}$ 

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2003as:\*
geneseqp2003bs:\*
geneseqp2004s:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Aab69496 Ricinus c	-										٠.	_	Aab79181 Corynebac		_			Abg24250 Novel hum	Aab69505 Methanoco		Aab69504 Methanoco	Abg24252 Novel hum	Abu49254 Protein e	Abg21490 Novel hum
SUMMARIES	Ę	111	AAB69496	AAB69495	AAB69503	ABP79052	AAB69501	AAB69497	AAB69498	AAG93226	ADA34150	AAB69502	AAB69499	AAB69500	ABG24254	AAB79181	ABB54937	ABP03233	ABB49279	ABG24253	ABG24250	AAB69505	ABG26219	AAB69504	ABG24252	ABU49254	ABG21490 .
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d	Query Warch	march	100.0	91.4	55.0	54.5	50.5	49.6	49.3	48.6	46.1	45.9	45.1	44.5	44.1	43.2	39.1	38.7	37.3	32.9	32.9	32.0	28.5	27.6	21.5	15.2	14.0
	9	י מכסד	557	509	306.5	303.5	281.5	276.5	274.5	270.5	256.5	255.5	251	248	245.5	240.5	218	215.5	207.5	183	183	178	159	153.5	120	84.5	78
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ABP30163 ABP25678 ABU21334	Abb6y532 AAY43982 AAY43981 AAR67385	ABP28230 ABP41194 ADE:24811	ABU49927 ABB55204 AAR04713	AAW01657 AAW14946 AAW12345	AAW56120 AAY23926 AAY93334 AAB11756
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256 27 28	30 30 31 31 31	3 3 3 5 4 3	333	3.6 4.4 1.0 1.0	4444 5443

## ALIGNMENTS

AAB69496 standard; protein; 113 AA. Ricinus communis PII protein. (first entry) 23-APR-2001 AAB69496; RESULT 1 AAB69496 

Castor bean, PII, plant nitrogen regulatory gene, P-PII; nitrogen assimilation; transgenic plant; herbicide screening

Ricinus communis.

US6177275-B1.

23-JAN-2001.

97US-00899330. 23-JUL-1997; 96US-0022328P. 24-JUL-1996;

Coruzzi GM, Lam H, Hsieh M; (UYNY ) UNIV NEW YORK STATE.

WPI; 2001-158572/16. N-PSDB; AAF58582, AAF58584.

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 1; Fig 1; 35pp; Bnglish.

The present sequence is encoded by a nitrogen regulatory PII gene. Movel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

Sequence 113 AA;

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23-JUL-1997;
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                                                                              23-APR-2001
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                        Gaps
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                                                                                          61 KWEIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKAE 113
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Score 557; DB 4; Length 113; Pred. No. 1.2e-57; O: Mismatches O; Indels
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Pred. No. 5.4e-52;
4; Mismatches 7; Indels
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100.0%;
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90.3%;
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                          113; Conservative
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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                                                                                                                                                                                            Synechococcus strain PCC 7942 PII protein.
AAB69503 standard; protein; 112 AA
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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in
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                                                      Novel P-PII genes capable of requiating plant nitrogen assimilation,
                                                                    useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
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nitrogen assimilation; transgenic plant; herbicide screening.
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Pred. No. 3.8e-25;
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49.1%; Pred. No. s.c.
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Best Local Similarity 49.13
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lam H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-158572/16
                  WPI; 2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in recoids ABPR16736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                           New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.5%; Score 303.5; DB 6 54.5%; Pred. No. 1.1e-27; iive 25; Mismatches 24
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                                                                                                                                                                                                                                Masignani V, Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Azospirillum brasiliense PII protein.
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 528; 815pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hsieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0022328P
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                                                                                                                                                       12-FEB-2031; 2001GB-00003424.
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(first entry)
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les 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azospirillum brasilense
    Neisseria gonorrhoeae
                                                                                                                                                                                                                                    Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lam H,
                                                                                                                                                                                                                                                                        WPI; 2003-058415/05.
                                                                                                                                                                                           (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                          N-PSDB; ABZ40022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                        WO200279243-A2
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                                                                                                                   12-FEB-2002;
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                                                                                                                                                                                                                                  Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2003
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                                                                            10-OCT-2002
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Matches
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transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                    KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSBFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                         EIVVSKDQVEDVIEKIIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                             Escherichia coli; PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                             DB 4; Length 112;
                                                                                                                                                                                                Indels
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49.3%; Score 274.5; DB 4;
Best Local Similarity 50.0%; Pred. No. 2.5e-24;
Matches 55; Conservative 25; Mismatches 29;
                                                                                                                                                                                                  28
                                                                                                                                                             49.6%; Score 276.5; DB 4
50.0%; Pred. No. 1.5e-24;
iive 26; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB69498 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example, Fig 1, 35pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00899330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli PII protein
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                                                                                                                                                                                                    55; Conservative
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                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
                                                                                                                               Sequence 112 AA;
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                                                                                                                                                                                   Best Loc
Matches
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent electronic form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides derived from Coryneform bacteria, for identifying
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                                                                                                                                                                                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                           Ξ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.6%; Score 270.5; DB 4; Length 112; 45.0%; Pred. No. 7.5e-24;
                                                           BIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6980; 246pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Ozaki A;
                                                                                                                                                                                                                                                                 C glutamicum protein fragment SEQ ID NO: 6980.
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Ikeda M,
                                                                                                                                                                       AAG93226 standard; protein; 112
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03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000EP-00127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum
                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-376931/40.
N-PSDB; AAH68445.
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07-APR-2000;
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Best Local Si
Matches 499
                                                                                                                                                                                                    AAG93226;
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Tateishi
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                                                                                                                                          RESULT 8
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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nuclectide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                    Rhodobacter capsulatus; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EMVLPDEMVDIAIEAIVGAARTEKIGDGKIFVSSIEQAIRIRIGEEGEDA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 112;
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47.3%; Pred. No. 4.4e-22;
tive 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium leguminosarum PII protein.
Rhodobacter capsulatus PII protein.
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                                                                                                                                                                                                                                                                                                                                                   Hsieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00899330.
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                                                                                                  Rhodobacter capsulatus.
                                                                                                                                                                                                                                                                                                                                                 Coruzzi GM, Lam H,
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-158572/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB69499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 VTAIVXPFKLDDVREALSDIGVQGITVTEVKGFGRHKGHTELYRGAEYVVD-FLPKVKIB 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VEALLRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                   baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Fri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 IVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VIISDAQAEEVINIIVETARIGKVGDGKVWMTNIEELVRVRTGERGEAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.1%; Score 256.5; DB 6
48.6%; Pred. No. 3.8e-22;
tive 22; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; SEQ ID NO 5437; 328pp; English
                                                                                                                                                                                                                             Acinetobacter baumannii protein #1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB69502 standard; protein; 112 AA.
                                                                                                    ADA34150 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THERAPEUTICS CORP.
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                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Conservative
                                                                                                                                                                                                                                                                                                                               Acinetobacter baumannii.
                                                                                                                                                                                                                                                                                       plant biocontrol agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daumannii protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADA30024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME
                                                                                                                                                                                                                                                                     Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-JUN-1998;
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                                                                                                                                                                                    20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                      JS6562958-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breton G,
                                                                                                                                             ADA34150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB69502;
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RESULT 10

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AAB69502

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Gaps

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Gaps

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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen sasimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of 11. The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                              3 KIRALIKPFKLDEVRS-LSGVGLQGITVTEAKGFGRQKGHTDLYRGAEYIVD-FLPKVXI 60
                                                                                                                                                                                                                                                                                                                                                                                       3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRIGERG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.5%; Score 248; DB 4; Length 111; 46.7%; Pred. No. 3.4e-21; tive 26; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 54613; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #24245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG24254 standard; protein; 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĭ,
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.7
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AASB8441.
                                                                                                                                                                                                                                                      Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                        The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVRM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bradyrhizobium japonicum; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                    Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A5.1%; Score 251; DB 4; Local Similarity 47.7%; Pred. No. 1.5e-21; hes 51; Conservative 27; Mismatches 27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB69500 standard; protein; 111
                                                                                                                                                                                                                                                                                     Example; Fig 1; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hsieh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00899330
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       96US-0022328P.
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                                                   (UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lam H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-158572/16
                                                                                                 Lam H,
                                                                                                                                          WPI; 2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1997;
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       24-JUL-1996;
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                                                                                                 Coruzzi GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2001
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RESULT 12

AAB69500

Matches

g à g

Example, Fig 1; 35pp; English

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                    of sites expressing (II). (I) and (III) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent din not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; proteinogenic amino acid; proteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; diagnosis; corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are neeful for forting.
                                                                                                                                                                                                                                                                                              4 VEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKME
                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; homeostasis; adaptation; HA protein;
                                                                                                                                                                                                                                                                                                                                                        64 IVVSKDQVEDVIEKIIEBARTGEIGDGKIFLLPVSDVIRVRTGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                          Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum HA protein sequence SEQ ID NO:318.
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                    44.1%; Score 245.5; DB 4
44.0%; Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                  30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB79181 standard; protein; 89 AA
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99DE-01032922.
99DE-01032924.
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99DE-01031636.
99DE-01032125.
99DE-01032126.
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99DE-01032930.
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99DE-01032935.
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99DE-01032128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                 1 Similarity 44.0
                                                                                                                                                                                                        Sequence 160 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB79181;
                                                                                                                                                                                                                                    Query Match
Best Local 8
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis
and adaptation (HA) proceins given in AAB79023 to AAB79242. The C.
and adaptation (HA) proceins given in AAB79023 to AAB79242. The C.
glutamicum HA genes (I) can be used in vectors for expression in host
cells and production of fine chemicals, such as, an organic acid,
proteinogenic or nonproceinogenic amino acid (preferred), purine or
pyrimidine base, nucleoside, lipid, saturated or unsaturated
fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor,
calveride or enzyme. The amino acids produced can be lysine, glutamine,
cysteine, valine, leucine, isoleucine, arginine, prodine, methionine,
cysteine, valine, leucine, isoleucine, arginine, prodine, histidine,
tyrosine, phenylalanine, or tryptophan. The fine chemical production can
be modulated. The presence of (I) or HA proteins encoded by then are used
for diagnosing the presence or activity of Corynebacterium diphtheriae.
(I) can be used to map the C. glutamicum genome or can be used as markers
for genetically engineered Corynebacterium or Brevibacterium. The HA
c proteins encoded by the (I) are used to maintain homeostasis in C.
glutamicum or help the microorganism to adapt to different environmental
                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                                                                                                      Schroeder H, Zelder O, Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 240.5; DB 4; Length
Pred. No. 2e-20;
5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 TGEIGDGKIFLLPVSDVIRVRTGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||::||||::|
|GKVGDGKVWMTNIEELVRVRTGERGEAA
                                                                                                                                                                                                                                                                                                                           Claim 20; Page 563; 712pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB54937 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.2%; Scor
49.4%; Pre-
tive 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis protein glnB.
99DE-01033006.
99DE-01041378.
99DE-01041379.
99DE-01041390.
99DE-01042088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Conservative
                                                                                                                                                      Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                        2001-061974/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                        N-PSDB; AAF71296
                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 89 AA;
                                                                                                                      (BADI ) BASF
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                   31-AUG-1999;
31-AUG-1999;
                                                     31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2003
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001
                                                                                   03-SEP-1999
                                                                     31-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                             enzymes.
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New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                   Sorokine A, Renault P, Ehrlich SD;
                                                                                                        Claim 6; SEQ ID NO 1639; 2504pp; French.
                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
       11-APR-2000; 2000FR-00004630.
                      11-APR-2000; 2000FR-00004630
                                                                  WPI; 2002-043418/06.
                                                    Bolotine A,
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB3300-ABB5561). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related acid sequence, particularly to identify Lactococcus lactis or related in lactic bacterian of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent electronic format directly from WIPO at the wipo.int/pub/published 18-OCT-2001) which is available in standardise OS field) 3 KVEAILRPWRVSQVSSALLKIG-IRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVK 61 2; Gaps 39.1%; Score 218; DB 5; Length 112; 43.2%; Pred. No. 1.2e-17; tive 24; Mismatches 37; Indels Query Match
Best Local Similarity 43.2%
Matches 48; Conservative Sequence 112 AA;

|:|||:| :::|| |::|:| |::|:|
| KIEAIIRTDKLEDLKAALSDNGLVHGWIVSQVLGYGEQKFTEYVRGQRI-ETTLLSKLK 61 62 MEIVVSKDQVEDVIBKIIBEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA 112 

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completed: May 24, 2004, 19:13:03 ne : 52 secs Search co

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 24, 2004, 19:10:08; Search time 14 Seconds (without alignments) 776.403 Million cell updates/sec

Title:

JS-09-756-541-2 557 Perfect score:

1 FYKVEAILRPWRVSQVSSAL......LLPVSDVIRVRTGERGDKAE 113 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		*				
Result No.	Score	Query Match	Query Match Length	DB	ΙD	끍
1 4	509	91.4	196	10	DB5024	i ki
8	315.5	56.6	112	Ċ	AH2095	nitrogen regulator
٣	4.	56.5	112	Ċ	F70310	
4	303.5	54.5	112	7	H81961	
S	302.5	54.3	112	7	B81019	
9	300.5	•	112	N	A39696	
7	281.5	50.5	112	7	S13078	
80		50.0	112	~	S73175	
σ	278.5	50.0	112	7	AF0354	
10	277.5	49.8	114	7	D82102	
11	276.5	9.65	112	7	S04377	nitrogen regulator
12	- 1	49.3	112	Н	RGECP2	nitrogen regulator
13	274.5		112	7	C91056	hypothetical prote
14		•	112	7	GB5900	hypothetical prote
15	274.5	49.3	112	7	AH0826	
16	276.5	48.6		ď	S52328	
17	269.5	48.4		N	S33180	
18	268.5	48.2	112	7	F64062	
19	268.5	48.2		N	AB2794	
20	268.5	48.2	157	7	A97573	
21	267.5	48.0	112	N	C87493	
22	266.5	47.8	112	7	AD3374	
23	265.5	47.7	121	C1	B82302	
24	264.5	47.5	112	C	C64307	probable nitrogen
25	260.5	46.8		N	G64467	nitrogen regulator
26	260.5	46.B		N	G70747	
27	253.5	45.5		N	D82985	
28		45.2	112	N	B69468	
29	251.5	45.2	112	N	T35668	nitrogen regulator

nitrogen regulator	glnK protein (AJ00	nitrogen regulator	nitrogen regulator	nitrogen regulator	nitrogen regulator										
B26567	D69188	H82631	AB0560	A33600	S76404	AG0381	B64775	H90691	D85542	AD2915	G97689	B69188	D87415	H87313	G86823
7	7	N	(7	7	~	7	7	~	7	7	2	0	N	N	N
111	115	112	112	111	85	112	112	112	112	116	116	115	112	114	113
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45.1	44.8	44	44.	44.	44	44	44	4.4	44.	43.	43.	43.	42,	42	39
251 45.1			248.5 44.						245.5 44.						

### ALIGNMENTS

RESULT 1 D85024	P II nitrogen sensing protein GLB I [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-reb-2001 C;Accession: D85024 D-snowners The Euronean Union Arabidonsis Genome Sequencing Consortium, The Cold Sprir	K;anonymous, The buropean Union Arabidopsis Genomes Sequencing Consolition, and Cold of Nature 402, 769-777, 1999 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198	A,Accession: DS5024 A,SCaute: preliminary A,Molecule type: DNA A,Residues: 1-196 <sto> A,Cross-references: GB:NC_001268; NID:g7268574; PIDN:CAB80683.1; GSPDB:GN00140 C,Genetics: A,Gene: AT4g01900 A,Map position: 4</sto>	Query Match 91.4%; Score 509; DB 2; Length 196; Best Local Similarity 90.3%; Pred. No. 6.2e-40; Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	OY 1 FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV 60	
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# RESULT 2 AH2095

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nitrogen regulatory protein P-II glnB [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. strain PCC 7120
C,Accession: AH2095
C,Accession: AH2095
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A,Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Reference number: AB1807; MUD:2159285; PMID:11759840
A,Recession: AH2095
A,Rocession: AH2095
A,Rotelus: Preliminary
A,Ro

Indels

ch 56.6%; Score 315.5; DB 2; 1 Similarity 58.2%; Pred. No. 2.7e-22; 64; Conservative 22; Mismatches 23;

Query Match Best Local 9

63

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RESULT 3

C; Superfamily: regulatory protein P-II

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nitrogen regulatory protein p-II NWB1995 [similarity] - Neisseria meningitidis (strain] C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Accession: B81019
R: Pattellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.: Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.: H; Qin, H.; Qumathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; V.
A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: AB1000; MUID: 2017575; PMID: 10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Synechococus sp.
C;Species: Synechococus sp.
C;Species: Synechococus sp.
C;Date: 008-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 26-Aug-1999
C;Date: 008-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 26-Aug-1999
C;Accession: A39696; F56817
R;Tsinoremas, N.F.; Castets, A.M.; Harrison, M.A.; Allen, J.F.; Tandeau de Marsac, N.
R;Tsinoremas, N.F.; Castets, A.M.; Harrison, M.A.; Allen, J.F.; Tandeau de Marsac, N.
A;Title: Photosynthetic electron transport controls nitrogen assimilation in cyanobacte:
A;Reference number: A39696; MUID:91271233; PMID:1905010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Rolidues: 1-112 <TET>
A;Cross-references: GB:AE002548; GB:AE002098; NID:g7227249; PIDN:AAF42322.1; PID:g72272:
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors translated the codon CCT for residue 83 as Thr R;Li, N.; Warren, P.V.; Golbeck, J.H.; Frank, G.; Zuber, H.; Bryant, D.A.
Biochim. Biophys. Acta 1059, 215-225, 1991
A;Title: Polypeptide composition of the Photosystem I complex and the Photosystem I cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrogen regulatory protein P-II - Synechococcus sp. (strains PCC 7942 and PCC 6301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
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    Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%; Score 302.5; DB 2
53.6%; Pred. No. 4.4e-21;
iive 26; Mismatches 24
; Score 303.5; DB 2; Pred. No. 3.5e-21; 25; Mismatches 24
             54.5%;
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                                                                                        60; Conservative
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             Query Match
Best Local Similarity
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A,Molecule type: DNA
A,Residues: 1-112 <TSI>
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Best Local Si
Matches 59
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A,Experimental source: strain VF5
C,Genetics:
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A;Experimental source: serogroup A, strain Z2491
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R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, F. Plotroy, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: F70310
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998

Aritie: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

Aritie: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

Arecession: F70310

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C;Species: Aguifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Weisseria meningitidis
C,Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                  3 KVEALIRPFKLDEVKIALVNAGIVGMTVSEVRGFGRQKGQTERYRGSBYTVB-FLQKLKV
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                                                                                                                                                  1; Gaps
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Indels

21;

59; Conservative

Matches

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RESULT

Query Match Best Local Similarity

56.5%; Score 314.5; DB 2 53.6%; Pred. No. 3.4e-22; 29; Mismatches

Superfamily: regulatory protein P-II Keywords: phosphoprotein; signal transduction 51/Binding site: UMP (Tyr) (covalent) #status predicted

A;Gene: glnB C;Superfamily, C;Keywords: pt F;51/Binding a

C:Superfamily: regulatory protein P-II C:Keywords: phosphoprotein F;51/Binding site: UMP (Tyr) (covalent) #status predicted

A; Gene: glnB; NMA0447

A; Molecule type: DNA A; Residues: 1-112 < PAR>

A;Status: preliminary A; Accession: H81961

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nitrogen regulatory protein P-II [similarity] - Vibrio cholerae [strain N16961 serogroup C; Species: Vibrio cholerae C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 24-Aug-2001 C; Accession: D82102 R; Period N.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; P; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitrogen regulatory protein P-II glnB [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0354
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                        A, Experimental source: strain Avonport
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
Plant Mol. Biol. Rep. 13, 333-335, 1995
A;Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
A;Reference number: S73108
A;Accession: S73175
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A,Reference number: AB0001; MJID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSBDKFVAKVKM
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                                                                                                                     A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-112 <REI>
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                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: regulatory protein P-II
C;Keywords: chloroplast; phosphoprotein; signal transduction
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 278.5; DB 2;
49.1%; Pred. No. 7.2e-19;
iive 29; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 278.5; DB 2; 52.7%; Pred. No. 7.2e-19; tive 21; Mismatches 30;
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Matches 58; Conserv
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A;Molecule type: DNA
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Mol. Gen. Genet. 224, 421-430, 1990
A;Title: Characteerization of three different nitrogen-regulated promoter regions for the
A;Reference number: S13078; MUID:91094780; PMID:1702507
A;Accession: S13078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Description: P-II protein synthesis is increased under conditions of nitrogen fixation C,Superfamily: regulatory protein P-II C,Keywords: phosphoprotein; signal transduction F;51/Binding site: UMP (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                           A,Description: involved in signal transdution
A,Note: modification state depends on the nitrogen source and the spectral light quality
C,Superfamily: regulatory protein P-II
C,Keywords: phosphoprotein; signal transduction
E,49/Bhinding site: phosphate (Ser) (covalent) #status predicted
F,51/Binding site: UMP (Tyr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nítrogen regulatory protein P-II - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C;Accession: S13078
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A;Experimental source: strain SP7
C;Genetics:
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                       A;Reference number: A56817; MUID:91355213; PMID:1653017
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49.1%; Pred. No. 3.8e-19;
tive 26; Mismatches 29;
                                                  A, Accession: F56817
A, Status: preliminary
A, Mecule type: protein
A, Residues: 1-40 < LII>
A, Experimental source: PCC 6301
C, Genetics:
C, Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
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Best Local S:
Watches 54
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Best Local
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Length 114;

Superfamily: regulatory protein P-II Keywords: phosphoprotein :53/Binding site: UMP (Tyr) (covalent) #status predicted

Map position: 1 A;Gene: VC2239

C; Genetics

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-114 <HEI>A;Cross-references: GB:AE004295;

Nature 406, 477-483, 2000

Indels

29; DB 2;

49.8%; Score 277.5; DB 2 50.0%; Pred. No. 9.1e-19;

Query Match Best Local Similarity 50.04 Matches 55; Conservative

셤 ð d

25, Mismatches

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A; Molecule type: DNA.
A; Molecule type: DIA.
A; Cross-references: GB: MiG778; NID: 9146165; PIDN: AAA23883.1; PID: 9146166
B; Van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, D.
A; Van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, D.
A; Van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, D.
A; Yairle: The genes of the glutamine synthetase adenylylation cascade are not regulated }
A; Reference number: S36284; MUID: 94018640; PMID: 8412694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Pathway: nitrogen regulation pathway A;Note: this protein participates indirectly in activation of glutamine synthase activit A;Note: this protein participates indirectly in activation of glutamine synthase expects. A;Note: under nitrogen-limiting conditions it is covalently uridylylated; in nitrogen extransferase / uridylyl-removing enzyme which is regulated by the glutamine/alpha-ketogli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: de-uridylylated P-II forms a complex with nitrogen regulation protein II the uridylylated form of P-II does not complex with ntrB; free ntrB phosphorylates nitro A; Note: phosphorylated nitrogen regulation protein I (ntrC) activates transcription of I
                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:S67014; NID:g455660; PIDN:AAB28779.1; PID:g455663
A;Note: sequence extracted from NCBI backbone (NCBIN:139878; NCBIP:139882)
A;Note: sequence extracted from NCBI backbone (NCBIN:139878; NCBIP:139882)
A;Note: sequence extracted from NCBI backbone (NCBIN:139878; NCBIP:139882)
Mol. Gen. Genet. 226, 49-58, 1991
A;Title: Isolation and nucleotide sequence of the hmp gene that encodes a haemoglobin-1: A;Reference number: S15991; MUID:91238719; PMID:2034230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rison, H.S.; Rhee, S.G.
7. Biol. Chem. 262, 8699-8695, 1987
A.Title: Cascade control of Escherichia coli glutamine synthetase: purification and proj
A.Reference number: A29307; MUID:87250488; PMID:2885322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-112 <BLAT>
A;Cross-references: GB:AE000341; GB:U00096; NID:g1788899; PIDN:AAC75606.1; PID:g1788904
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Description: uridylylated P-II forms a complex with adenylyltransferase; this complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ylytransferase deadenylylates glutamine synthase
AlNote: free glutamine synthase is active; adenylylated glutamine synthase is inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain K-12, substrain W3110
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Kiley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
C;Date: 30-Jun-1988 #sequence revision 10-Nov-1995 #text change 01-Mar-2002 C;Accession: C49940; S15991; A29307; S37753; H65032; S31961
R;Liu, J.; Magasanik, B.
J. Bacteriol. 175, 7441-7449, 1993
A;Title: The glnB region of the Escherichia coli chromosome.
A;Reference number: A49940; MUID:94042920; PMID:8226691
A;Accession: C49940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-112 <VAS>
A,Cross-references: GB:X58872; NID:941730; PIDN:CAA41683.1; PID:941732
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A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
A,Accession: H65032
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C;Keywords: phosphoprotein; signal transduction
F;51/Binding site: UMP (Tyr) (covalent) #status experimental
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1 Similarity 50.0%; Pred. No. 1.7e-18;
55; Conservative 25; Mismatches 29;
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A; Residues: 1-112 <LIU>
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A;Residues: 1-12 <VAN>
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C,Function: <GEN>
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                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004295; GB:AE003852; NID:g9656789; PIDN:AAF95383.1; GSPDB:GNO01
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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                                                     A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Feference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82102
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C;Species: Klebsiella pneumoniae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C;Accession: S04377
F;Holtel, A.; Merrick, M.
Mol. Gen. Genet. 215, 134-138, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Holtel, A.; Merrick, M. Mol. Genet. 215, 134-138, 1988
Mol. Genet. 215, 134-138, 1988
A;Title: Identification of the Klebsiella pneumoniae glnB gene: nucleotide A;Reference number: S04376; MUID:89201233; PMID:2907369
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A;Molecule type: DNA
A;Residues: 1-112 <HOL>
A;Residues: 1-112 <HOL>
A;Crose-references: EMBL:X14012; NID:g43804; PIDN:CAA32177.1; PID:g43806
A;Experimental source: strain M5a1
C;Genetics:
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C,Species: Escherichia coli
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DB 2; Length 112;

49.6%; Score 276.5; DB 2 50.0%; Pred. No. 1.1e-18;

26; Mismatches

Conservative

Query Match Best Local Similarity

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ted, these events are reversed C.Superfamily: regulatory protein P-II C.Keywords: phosphoprotein; signal transduction F.51/Binding site: UMP (Tyr) (covalent) #status predicted

A,Gene: glnB C,Function:

28; Indels

RESULT 12

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112

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nitrogen regulatory protein p-II STY2808 [imported] - Salmonella enterica subsp. enteric c; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0826 C;Accession: AH0826 C;Accession: AH0826 C;Accession: Aping C;Accession: A;Pougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
A;Anthore: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <-PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02764.1; PID:g16503774; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
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EIVVSKOQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA.
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 24, 2004, 19:15:40
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C,Superfamily: regulatory protein P-II
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Best Local Similarity 50.0%
-hag 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AH0826
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           63
                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉱
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A./Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A./Actession: G85900
A./Actaus: preliminary
A./Actession: G85900
A./Actaus: Draiminary
A./Actession: G85900
A./Estaus: Davis Mallo (157:H7); Substrain EDL933
                                                                                                                                                                                                                                                                                                                                               몺
                                                                                                                                                                                                                                                                                                                                                    Ciperies: Escherichia coli
CiDate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
CiAccession: C91056
Ribayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Trile: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc. A;Reference number: A99629; MuID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                  - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KVERILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSBFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                        62
                                                                  KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRQGGSEFSEDKFVAKVKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 EIVVPDDIVDTCVDTIRTAQTGKIGDGKIFVEDVARVIRIRTGEEDDAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 49.3%; Score 274.5; DB 2; Length 112; 1 Similarity 50.0%; Pred. No. 1.7e-18; 55; Conservative 25; Mismatches 29; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                   63 EIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLÞVSDVIRVRIGERGDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.3%; Score 274.5; DB 2
Best Local Similarity 50.0%; Pred. No. 1.7e-18;
Matches 55; Conservative 25; Mismatches 29
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;Superfamily: regulatory protein P-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: ECS3419
C;Superfamily: regulatory protein P-II
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-112 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
G85900
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Gaps

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GenCore version 5.1.6
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procein search, using sw model OM protein May 24, 2004, 19:06:17; Search time 10.5 Seconds Run on:

(without alignments) 560.374 Million cell updates/sec

1 FYKVEAILRPWRVSQVSSAL......LLPVSDVIRVRTGERGDKAE 113 Title: Perfect score: Sequence:

**BLOSUM62** 

Scoring table:

US-09-756-541-2

141681 seqs, 52070155 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 0B Minimum | Maximum |

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ID Description	GLNB NOSPU 030794 nostoc punc	AQUAE 066513	FREDI Q47894		SYNP7 P80016		-	PORPU P51254		ECOLI P05826	RHORU Q53044	, ,				METJA 060381	p14179	_	METUA 058740 1	P13556	Q9tm37	HILV P09827	026760	COL1 P3850	GINI_WEFFER		RHIET 054053	O54053	054053 007428	054053 007428 P54809	ACSU 0054053 ACSU 007428 ETBA P54809 ETBA F54806	HIET 054053 ACSU 007428 ETBA P54809 ETBA P54809 ETBA P25806 ETIL P25770	METTE 054053  BACSU 007428  METTBA P54806  METTL P25770  METTL P71525	HIET 054053 ACSU 0540438 ETER 0540438 ETTL P54806 ETTL P55770 ETMP P51525
DB	 	44	Н	н	Н	-	-	H	-	7	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	٦	۲	۲	Н	Н	,	4	-11	444	444	4444			
iength	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	112	113	111	115	112	115	112		116	116	116	116 123 125	116 123 125 128	116 123 125 128 128	116 123 125 128 121 121
* Query Match Length	56.6	•		12	55.0	Н	50.5	50.0	49.6	49.3	48.6	48.4	48.4	48.2	48.0	47.5	46.8	46.8	•	45.9		45.1		44.1	43.7	41.7		'n	'n.	5.2	0.5.5	9 9 9 5	9,000,9	999999
Score	315.5	314.5				286.5		278.5			٠					264.5	260.5	260.5	260.5	255.5	254.5	251	249.5	245.5	243.5	232.5		195.5	195.5	185.5	195.5 181.5 170.5	195.5 181.5 170.5 167.5	185.5 181.5 170.5 167.5	185.5 181.5 170.5 167.5 166
Result No.		N	m	4	Ŋ	9	7	8	on	10	11	12	13	*	15	16	17	18	19	20	21	22	23	24	25	26	1 (		7.7	28	2 8 7 2 8 7	27 28 30 30	3 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

56.6%; Score 315.5; DB 1; Length 112; 58.2%; Pred. No. 1e-22;

Best Local Similarity

Query Match

Q50787 methanobact P25771 methanococc	Q50786 methanobact P54808 methanosarc	P71524 methanococc	Q7tug9 prochloroco	Q07981 helix asper Q9z309 mus musculu	Q50715 mycobacteri	075838 homo sapien	P10809 nomo sapien
GLN2 METTM GLN1 METTL	GLN1_METTM GLN1_METBA	GLINI_METIMP	GLN3 METBA GSHB PROMP	FAR1_HELAS KIP2_MOUSE	IMDH_MYCTU	KIP2_HUMAN	CH60_HUMAN
нн	нн	н.			Н	Н	Н
121	105	105	307	305	529	187	573
28.5	26.8	25.2	24.3 14.3	13.6	13.0	12.9	12.7
159	149.5	140.5	135.5	75.5	72.5	72	70.5
9. 9. 4. 13.	36	38	3 0 0 0	41	43	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                             ARAINEAUCE 29133 / PCC 73102;

KEAIN-ATCC 29133 / PCC 73102;

KEDLINE-98304077; PubMed-9639924;

KEDLINE-98304077; PubMed-9639924;

KEDLINE-98304077; PubMed-9639924;

KEDLINE-98304077; PubMed-9639924;

KETAIN ATCC 29133; GluB or the PII protein may be essential.";

KI ARAINEATC 29133; GluB or the PII protein may be essential.";

KI MICROPIOLOGY 144:1537-1547(1998).

C -1- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS GENE (GLNA). P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF NR-1 TO NR-1-POSPHORYLATED THESE EVENTS ARE REVERSED (BY SIMILARITY).

C -1- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN TO 2-KETOGLITARATED BECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS THE DEADENLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENDERNIT: HOMOTIME (BY SIMILARITY).

C -1- FUNCTION: THE ENDERNITATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENDERNIT: HOMOTIME (BY SIMILARITY).

C -1- PIM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL LIGHT QUALITY (BY SIMILARITY).
                                                                          15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRUD340; rise....

ProDom; PD001194; PII GIAB; 1.

PROSITE; PS00496; PII GIAB UMP; 1.

PROSITE; PS00638; PII GIAB CTER; 1.

Transcription regulation; Nitrogen fixation; Phosphorylation.

Transcription PROBABLE).

49 PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                     Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9C2224C38B67583A CRC64;
                     112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, PO5826; 2PII.
INLECTPO: IPRO02131; PII_GlnB.
INLECTPO: IPRO0332; PII_GlnB_UMP_S.
Pfam; PP00543; P-II; 1.
                                                               (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF017419; AAC26348.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00340; PIIGLNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA;
                                                                                                                                                                        Nostoc punctiforme
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI TaxID=63737;
                                                               15-DEC-1998
15-DEC-1998
15-JUL-1999
                     GLNB NOSPU
030794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
GLNB_NOSPU
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3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05826; 2PII
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1197;
                                                                                                                                                                                         GLNB FREDI
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                                                                                                                                                          RESULT 3
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                                          3 KVEAILRFWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
                                                             Nature 392:353-358(1998).

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLM

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLM. P-

TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYL/LATED TO P-II-UMP. P-

II-UMP ALLONS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS),

THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-II

IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert G., Warrer P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.B., Owerbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, F70310; F70310; PROSESS, 2PII.
HSSP, P0525; 2PII.
InterPro; IPR002187; PII_GlnB_UMP_S.
PRINTS; PR05343; PII_GlnB_UMP_S.
PRINTS; PR053440; PIII; 1.
PRINTS; PR05496; PII_GlnB, 1.
PROSITE; PS00496; PII_GlnB, UMP; PALSE_NEG.
PROSITE; PS00638; PII_GLNB_UMP; PALSE_NEG.
                                                                                                         63 EIVVSKDQVEDVIEKLIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                          62 EIVVDDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRIRTGEKNTEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.5%; Score 314.5; DB 1; Length 112; llarity 53.6%; Pred. No. 1.3e-22; Conservative 29; Mismatches 21; Indels 1.
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homotrimer (By similarity). SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                               30.MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                 112 AA.
              22; Mismatches
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                Nitrogen regulatory protein P-II
GLNB OR AQ 109.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000674; AAC06473.1; -.
                 64; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                     GLINB AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                         STERIN=VF5
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AQUAE
                   Matches
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Gaps

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Best Local Similarity Matches 59; Conserv

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-!- SUBUNIT: Honotrimer (By Similarity).
-!- PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL LIGHT QUALITY (BY SIMILARITY).
-!- SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM
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                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 EIVVSKDQVEDVIEKIIEERARTGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                         Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
                                                                 63 BIVVSKDQVEDVIEKLIEBARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                              PRINTS; PROJECT FILE. 1.
PROSITE; PE001194; PII GINB UMP; 1.
PROSITE; PS00638; PII GINB UMP; 1.
PROSITE; PS00638; PII GINB CTER; 1.
Transcription regulation; Mirregen fixation; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 56.5%; Score 314.5; DB 1;
Best Local Similarity 57.3%; Pred. No. 1.3e-22;
Matches 63; Conservative 23; Mismatches 23;
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InterPro; IPR002332; PII_GlnB_UMP_S.
Pfam_ PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRQUENCE 112 AA; 12478 MW;
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62 EIVVDEGQVDMVVDKIVSAARTGBIGDGKIFISPVDSVVRIRIGEKDTBA EIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homotrimer (By similarity).
PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SCURCE AND SPECTRAL LIGHT QUALITY (BY SIMILARITY).
SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061201; PubMed=8905231; Kaneko T., Asamizu E., Nakamura Y., Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RES. 3.109-136 (1996)

FINCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
UR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY)
IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY)
TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS
THE DEADDRYLATATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                             MEDLINE-98088000; PubMed-9426594; Garcia-Dominguez M., Florencio F.J.; Garcia-Dominguez M., Florencio F.J.; "Witrogen availability and electron transport control the expression of ginB gene (encoding PII protein) in the cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitrogen requlatory protein P-II (PII signal transducing protein).
GINB OR SSL0707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%; Score 311.5; DB 1; Length 112; 55.5%; Pred. No. 2.5e-22; ive 25; Mismatches 23; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Nitrogen fixation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA; 12397 MW; F9ABD0F5C173B799 CRC64;
                                                                                                                                                                      Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom, PD001194, PII glnB; 1.
PROSITE, PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
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                    PRT;
                                                                                                                                                                                                                                                                                                                                              of ginB gene (encoding PII protein)
Synechocystis sp. PCC 6803.";
Plant Mol. Biol. 35:723-734(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X97496; CAA66127.1;
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PRINTS; PR00340; PIIGLNB.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                              NCBI TaxID=1148;
                    GLNB SYNY3
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GLNB_SYNY3
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Forchhammer K., Tandeau de Marsac N.;
"PhosphoryTation of the PII protein (glnB gene product) in the
"PhosphoryTation of the PII protein (glnB gene product) in the
cyanobacterium Synechococcus sp. strain PCC 7942: analysis of in
vitro kinase activity.";
J. Bacteriol. 177:5812-5817(1995).

-i- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PCC 6301;
MEDLINE=90249505; PubMed=2110911;
Harrison M.A., Keen J.N., Findlay J.B.C., Allen J.F.;
Harrison M.A., Keen J.N., Findlay J.B.C., Allen J.F.;
Modification of a glnB-like gene product by photosynthetic electron transport in the cyanobacterium Synechococcus 6301.";
PERS Lett. 264:25-28(1990).
                                                                                                                                                                                                                                                                                                                                                              "Photosynthetic electron transport controls nitrogen assimilation in cyanobacteria by means of posttranslational modification of the glnB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The PII protein in the cyanobacterium Synechococcus sp. strain PCC 1942 is modified by serine phosphorylation and signals the cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.A.;
                                                                    01-WAY-1991 (Rel. 18, Created)
01-WAY-1992 (Rel. 22, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Witrogen regulatory protein P-II (PII signal transducing protein)
                                                                                                                                                               Symechococcus sp. (strain PCC 7942) (Anacystis nidulans R2), and Symechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEPOSITE STATEMENT OF A STATEMENT OF A STRAINE PCC (11).

MEDLINE=91355213; PubMed=1653017;

Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., Bryant D

Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., Bryant D

In Prolypeptide composition of the Photosystem I complex and the Photosystem I core protein from Synechococcus sp. PCC 6301.*;

Biochim. Biophys. Acta 1059:215-225(1991).
                                                                                                                                                                                                                                                                                                                          Isinoremas N.F., Castets A.M., Harrison M.A., Allen J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genes required for c-type cytochrome biogenesis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 88:4565-4569(1991)
                                    112 AA
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Forchhammer K., Tandeau de Marsac N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PCC 7942;
MEDLINE=96011366; PubMed=7592328;
                                                                                                                                                                                                                                                                                        STRAIN=PCC 7942;
MEDLINE=91271233; PubMed=1905010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 176:84-91(1994).
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inoue K., Bryant D.A.;
                                                                                                                                                                                                                         NCBI_TaxiD=1140, 1139;
                                                                                                                                                                                                                                                                                                                                                  Tandeau de Marsac N.;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                               gene product.
                                    GLNB SYNP7
P80016;
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RESULT 5
GLNB_SYNP7
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Conservative

61;

Matches

Local Similarity

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Query Match
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGPGAQGGSTERQGGSEFSEDKFVAKVKW
                                                                                          PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SCURCE AND SPECTRAL
IR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GINA. WHEN P-II IS PHOSPHORYLATED, THESE BYENTS ARE REVERSED.
FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GIN J. PETCOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS THE DEADENVLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAY B.J., Zhang Q., Li L.L., Pauetian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLMA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 EIVVSKOQVEDVIBKIIEBARIGBIGDGKIFLLPVSDVIRVRIGBRGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELVVEDAQVDTVIDKIVAAARTGEIGDGKIFVSPVDQTIRIRTGEKNADA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 306.5; DB 1; Length 112; 56.4%; Pred. No. 7.2e-22; ative 21; Mismatches 26; Indels 1.
                                                                                                                                                                                                                                                                                                                                               PRINTS; PRC0340; PIIGLNB.
PRODOM, PD001194; PII_GlnB.1.
PROSITE; PS00496; PII_GlnB.UMP; 1.
PROSITE; PS00638; PII_GlnB.UMP; 1.
Transcription regulation; Nitrogen fixation; Phosphorylation.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                           B3 B3 T -> P (IN REF. 1; AAA27312)
112 AA; 12391 MW; 5F44B64CBFF3C559 CRC64;
                                                                                                                      -!- SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ... crr-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II.
Parer...
                                                                                                                                                                                                                                                                                                              Interpro; IPR002187; PII glnB.
Interpro; IPR002332; PII GlnB_UMP_S.
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                                                                                                                                                                                                                                          EMBL; AP079137; AAA27312.1; -. PIR, A39696; A39696. HSSP; P05876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                    -!- SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00543; P-II; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     PhosSite, P80016;
                                                                                                              LIGHT QUALITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECREASES, P-II IS URIDYLATED TO P-II-UMP, WHICH CAUSES THE DEADENTYLATION OF GLUTAMINE SYNTHETASE BY GLNE, SO ACTIVATING THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bozouklian H., Elmerich C.; "Mucleotide sequence of the Azospirillum brasilense Sp7 glutamine synthetase structural genee."; Bjochimie 68:1181-1187(2986).
-1- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Zamaroczy M., Delorme F., Elmerich C.; "Characterization of three different nitrogen-regulated promoter regions for the expression of glnB and glnA in Azospirillum
EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HWBL; ABLOGAS, ...
HWSP, P05826; 2PII.
INTERPO: IPR002187; PII_glnB.
INTERPO: IPR002332; PII_GlnB_UMP_S.
PFam; PF00543; P-II.; PII_GlnB.
ProDom; PD001194; PII_GlnB; 1.
PROSTIE; P800496; PII_GlnB HP; 1.
PROSTIE; P800638; PII_GlnB UMP; 1.
PROSTIE; P800638; PII_GlnB UMP; 1.
Transcription regulation; Nitrogen fixation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EIVVSKDQVEDVIEKIIBEARTGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 112;
                                                                                                                            -1. SUBUNIT: Homorrimer (By similarity).
-1. PTM: Uridylylated/deuridylylated by glnD (By similarity).
-1. SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.4%; Score 286.5; DB 1
52.7%; Pred. No. 5.2e-20;
iive 23; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) Nitrogen regulatory protein P-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE006236; AAK04088.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azospirillum brasilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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ID GLINB AZOBR
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58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                      PIR; S73175; S73175.
HSSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GINB KLEOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
GLNB_KLEOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLINB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $2 \ \frac{1}{2} \ \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
Eukaryota, Rhodophyta, Bangiophyceae, Bangiales, Bangiaceae, Porphyra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. Rep. 13:333-335(1995).

-i- PUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYMANED TO P-II-UMP, THESE EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYMATED TO P-II-UMP, WHICH CAUSES THE
       TO 2-KETOGLUTARATE DECREASES, P-II IS URIDXIXIATED TO P-II-UMP.

PII-UMP ALLOWS THE DEADENTLIMENTON OF GAUTAMINE SYNTHEIASE (GS), THUS ACTIVATING THE BEADENTLYIMENTON OF GAUTAMINE SYNTHEIASE (GS).

IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.

UNCTION: P-II INDIRECTIX CONTROLS THE RENSCRIPTION OF THE GS GENE (GINA). P-II PREVENTE NR-II CATALYZED CONVERSION OF THE GS NR II PREVENTEN NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GINA. WHEN P-II SURINITIALEND TO P-II-UMP, THESE EVENTS ARE REVERSED.

SUBUNIT: HOMOCLTIMEN (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the Porphyra purpurea chloroplast
    P-II IS URIDYLYLATED TO P-II-UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EIVVSKDQVEDVIEKIIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 51 UMP.
112 AA; 12371 MW; B6258EC9C4B63871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.5%; Score 281.5; DB 1
llarity 49.1%; Pred. No. 1.5e-19;
Conservative 26; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERMY PR00543; P-II; 1.
PRINTS; PR00340; PIGGINB.
PRODOM; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GINB UMP; 1.
PROSITE; PS00638; PII GINB CTER; 1.
Transcription regulation; Nitrogen fixation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, PO5826; 2PII.
InterPro, IPR002187; PII glnB.
InterPro, IPR002332; PII GlnB_UMP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X51499; CAA35867.1; -.
EMBL; M26107; -; NOT_ANNOTATED_CDS.
PIR; S13078; S13078.
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Reith M.E., Munholland J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyra purpurea.
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P51254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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MEDLINE=89201233; PubMed=2907369;

MEDLINE=89201233; PubMed=2907369;

MEDLINE=89201233; PubMed=2907369;

MIGHEL A., Merrick M.; Klebsiella pneumoniae glnB gene: nucleotide

"Identification of the Rull TOO P GLN

"Identification of GL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 EIVVSKDOVEDVIEKIIEBARTGEIGDGKIFLLPVSDVIRVRTGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRODOM; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
TRANSCRIPTION regulation; Mirrogen fixation; Chloroplast.
BINDING 12320 MW; 29416AA49FC37AI8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 278.5; DB 1; Length 52.7%; Pred. No. 2.9e-19; ive 21; Mismatches 30; Indels
                                                                            (BY SIMILARITY).
-!- SUBUNIT: Homotrimer (By similarity).
-!- SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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10-0CT-2003 (Rel. 42, Last annota
Nitrogen regulatory protein P-II.
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last seq
110-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U38804; AAC08140.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrogen regulatory protein P-II 1.
GIMB OR E2553 OR C3076 OR Z3829 OR ECS3419 OR STM2561 OR STY2808 OR
T0295 OR SF2600 OR S2772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Son H.S., Rhee S.G.; "Cascade control of Escherichia coli glutamine synthetase. Purification and properties of PII protein and nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holtel A., Merrick M.; Mebsiella pneumoniae glnB gene: nucleotide sequence of wild-type and mutant alleles."; Medl Gen. Genet. 215:134-138 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 EIVVSKDQVEDVIEKIIBEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.6%; Score 276.5; DB 1; Length 112; 50.0%; Pred. No. 4.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 50.0%; Pred. No. 4.4e-19; 55; Conservative 26; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       50 50 E-X: GLUTAMINE AUXOTROPHY.
112 AA; 12429 MW; CC15D58A2F225507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae, Escherichia.
NCBI_TaxID≍562, 217992, 83334, 602, 601, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 21, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                         ProDom; P0001194; FII gluB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Mitrogen fixation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA
                                                                                                                                                                                                                            naser rocce, IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          its structural gene.";
J. Biol. Chem. 262:8690-8695(1987)
[2]
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MEDLINE=87250488; PubMed=2885322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                      EMBL; X14012; CAA32177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli,
Escherichia coli O6,
Escherichia coli O157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                          Pfam; PFC0543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium,
Salmonella typhi, and
                                                                                                                                                                                         PIR; S04377; S04377.
HSSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best focal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigella flexmeri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=E.coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGEN
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GLNB_ECOLI
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Re SEQUENCE FOR N.A.

Re SHLINES-SISTBISTOR PROMECAZIONAL SHOW D.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR, PROMECAZIONAL SHOWS AND C.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR, PROMECAZIONAL SHOWS AND C.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR PROMECAZIONAL SHOWS AND C.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR PROMECAZIONAL SHOWS AND C.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR SHOWS AND C.C., LILLEY P.E., DIXON N.E., NEULINES-SISTBISTOR SHOWS AND C.C., LILLEY P.E., DIXON N.E., SEGUENCE STR. SHOWS AND C.C., DIXON N.E., SEGUENCE STR. SHOWS AND C.C., DIAGO-VIGEN SHOWS AND C.C., DECENA N.T., BULLAND V., SEGUENCE STR. SHOWS AND C.C., DIAGO-VIGEN SHOWS AND C.C., AND M.E., SEGUENCE STR. SHOWS AND C.C., DIAGO-VIGEN SHOWS AND C.C., NEW YORK OF SEGUENCE STR. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., NEW YORK SHOWS AND C.C., ALD H. B. SHOWS AND C.C., AND M.E. SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., AND M.E. SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., AND M.E. SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., SEGUENCE STR. SHOWS AND C.C., ALD H. B. SHOWS AND C.C., SEGUENCE STR. SHOWS
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15-DEC-1998
                                                                                                                                                                                                                       Cheah E., Ca
Ollis D.L.;
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SEQUENCE FROM N.A.
SPECIESS. S. TYPAIN-TY2 / ATCC 700931;
SPECIESS. S. TYPAIN: STRAIN-TY2 / ATCC 700931;
MEDLINE-22531367; PubMed=12644564;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                            SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterstor R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulation of transcription of the glnALG operon of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22272406; PubMed=12384590;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                     van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D., "The genes of the glutamine synthetase adenylylation cascade are not regulated by nitrogen in Escherichia coli."; Mol. Microbiol. 9:443-458 (1993).
                                                                                                                                                                                                                                                      "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-S. flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a, MEDLINE=22590274; PubMed=12704152; Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Pulmkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flexneri serotype 2a strain 2457T.";
Infect, Immun, 71:2775-2786(2003).
                             SPECIES=E.coli; STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES=S.typhi, STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
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Magasanik B.;
                                              MEDLINE=94018640; PubMed=8412694;
                 SEQUENCE OF 1-12 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:848-852(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the Escherichia coli signal transducing protein PII.";
                                                                                                                                                      Vasudevan S.G., Gedye C., Dixon N.E., Cheah E., Carr P.D., Suffolk P.M., Jeffrey P.D., Ollis D.L.; "Escherichia coli PII protein: purification, crystallization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Rhodospirillum.
NCHI_TaxID=1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johansson M., Nordlund S.;
Johansson M., Nordlund S.;
"Transcription of the gina and glnA genes in the photosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 BIVVSKDQVEDVIEKIIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95171116; PubMed=7866749;
Cheah B., Carr P.D., Suffolk P.M., Vasuvedan S.G., Dixon N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 49.3%; Score 274.5; DB 1; Length 112; I Similarity 50.0%; Pred. No. 6.8e-19; 55; Conservative 25; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the P(II) protein family.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). SPECIES=E.coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterium Rhodospirillum rubrum.";
Microbiology 142:1265-1272(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 11170 / SL;
MEDLINE=96254013; PubMed=8704966;
                                                                                                                 SPECIES=E.coli;
MEDLINE=94123764; PubMed=8293810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nitrogen regulatory protein P-II.
                                                                                  CRYSTALLIZATION, AND SUBUNITS.
by protein phosphorylation.";
Biochimie 71:1005-1012(1989).
                                                                                                                                                                                                                                                   oligomeric structure.";
FEBS Lett. 337:255-258(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structure 2:981-990(1994).
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Pfam; PF00543; P-II;
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P43519;
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GLNB RHOSE
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Godrie T., Goffeau A., Wann D., Kiss E., Lelaure V., Masuy D.,
A Halysis of the chromosome sequence of the legume symbiont
Sinchizohum meliloti srrain 1021.", Weidner S., Galibert F.;
Analysis of the chromosome sequence of the legume symbiont
Sinchizohum meliloti srrain 1021.", BB02 (2001).

The Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
TO 2-KETOGLIMARATE BECREASES, P-11 IS URIDKLYLATED TO P-11-UMP.
TO 2-KETOGLIMARATE BECREASES, P-11 IS URIDKLYLATED TO P-11-UMP.
TO 1-THOS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-11
SIS DEURIDYLATED AND PROMOTES THE ADMITMATION OF GS.
THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-11
SIS DEURIDYLATED AND PROMOTES THE TRANSCRIPTION OF THE GS.
C-1- FUNCTION: P-11 INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS.
C-1- FUNCTION: P-11 INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS.
C-1- FUNCTION: P-11 PREVENTES RN-11 CATALYZED CONVERSION OF NR-1 TO NR-1 TO NR-1 PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-11
    and for commercial
      oved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              63 BIVVSKDQVEDVIEKIIEEARIGEIGDGKIFILLPVSDVIRVRIGERGDKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arcondeguy T., Huez I., Fourment J., Kahn D.; "Symbiotic nitrogen fixation does not require adenylylation of glutamine synthetase I in Rhizobium meliloti."; FEMS Microbiol. Lett. 145:33-40(1996).
                                                                                                                                                                                                                                                                                                     DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                   PRINTS; PR00340; PIIGLMD.
PRINTS; PR00340; PII_GLMD.
ProDon;
PROSITE; PS00496; PII_GLMB_UMP; 1.
PROSITE; PS00638; PII_GLMB_CTER; 1.
PROSITE; PS00638; PII_GLMB_CTER; 1.
TRANSCRIPCION regulation, Nitrogen fixation.
Transcription regulation, Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.6e-18; 26; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GLNB OR R01639 OR SMC00947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
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         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                          48.6%; Score 270.5;
                        entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                   HSSP; PO5826; 2PII.
InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
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STRAIN=RCR2011 / SU47;
MEDLINE=97085050; PubMed=8931324;
                                                                                                                                                                                                                                                                                                                          48.2%;
                                                                                    AF029703; AAB84167.1;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.2%
Matches 53; Conservative
                                                                      EMBL; X84158; CAA58963.1;
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                                                                                           PIR; S52328; S52328.
HSSP; P05826: 2PTT
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GLNB RHIME
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;
"Nuclectide sequence and characterization of the Rhodobacter
sphaeroides glnB and glnA genes.";
Microbiology 140:2143-2151(1994).
-! FUNCTION: P-II INDIRECTLY COMTROLS THE TRANSCRIPTION OF THE
GLUTAMINE SYMTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED
CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL
ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLLATED TO P-II-UNP, THESE
BUCKRASES, P-II IS URIDYLYLATED TO P-II-UNP, WHICH CAUSES THE
DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRQGGSEFSEDKFVAKVKM
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01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Nitrogen regulatory protein P-II (PII signal transducing protein)
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Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00340; PliGLNB.
Probom; PD001194; Pli glub; 1.
PR051TE; P800496; Pli Glub UMP; 1.
PR051TE; P800436; Pli Glub UMP; 1.
Transcription regulation; Nitrogen fixation; Complete proteome.
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48.6%; Pred. No. 2e-18;
tive 27; Mismatches 27; Indel9 1;
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IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.-!- SUBUNIT: Homotrimer (By similarity).-!- SIMILARITY: Belongs to the P(II) protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MP (BY SIMILARITY)
85E6465E64B57001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, ALS91787; CAC46218.1; -.
HSSP, POG865; 2PII.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95005468; PubMed=7921264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ğ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 112 AA; 12281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U50385; AAC44623.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

-i- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN

-i- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN

TO 2-RETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP. P-

II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYMTHETAGE (GS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MARF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; Submitter T., Standa T., Shingo S., Sugimoto M., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Matsuno A., Matsuno M., Matsuno S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE (GLMA). P-II PREVENTS NR-II CATALYZED CONVERSION OF THE GS NR-I PROSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLXTATED TO P-II-UMP, THESE EVENTS ARE REVERSED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THUS ACTIVATING THE BNZYME. CONVERSERLY, IN NITROGEN EXCESS P-II SI DRURINIATED AND PROMOTES THE ADENYLATION OF GS (BY CELLY PROPERTY.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KIVVSKDQVEDVIBKIIBEARIGEIGDGKIFILPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 EVVVPDELVDQCIEAIIETAQTGKIGDGKIFVYHVBRAIRIRTGEENEDA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Mirogen fixation; Complete proteome.

Transcription regulation; Wip (BY SIMILARITY).

SEQUENCE 112 AA; 12640 MW; B8CD67EFA9381D61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.2%; Score 268.5; DB 1, 49.1%; Pred. No. 2.5e-18; tive 24; Mismatches 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERNYS; PRO0543; P-II; 1.
PRINYS; PRO0340; PIIGLMB: 1.
PRODOM; PD0001194; PII_GLMB: 1.
PROSITE; PS00496; PII_GLMB_UNP; 1.
PROSITE; PS00638; PII_GLMB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB_UMP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrogen regulatory protein P-II. GINB OR MLL0345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98NI8;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                 EMBL; U32718; AAC21999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                 F64062; F64062.
                                                                                                                                                                                                                                                                                                                           HSSP; P05826; 2PII.
TIGR; HI0337; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=381;
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                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKOM
                             is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Mcriavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh M., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heddlow E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 EIVVSKDOVEDVIEKIIEBARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EVVLADDMVEAAVEALVSASRIDKIGDGKIFISPVEQAIRIRTGETGEDA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCNIT: Homotrimer (By similarity).
-!- PTM: Uridylylated/deuridylylated by glnD (By similarity).
-!- SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Indels
                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROCESTOR PRIGENB.
PRODOM; PROCESTOR PRIGENB. 1.
PROSITE; PROCESTS; PRICENB. 1.
PROSITE; PROCESS; PRICENB. CTER; 1.
PROSITE; PROCESS; PRICENB. CTER; 1.
PROSITE; PROCESS; PRICENB. CTER; 1.
PROBOGE PROCESS PRICESS PRICESS PROCESS PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%; Score 269.5; DB
46.4%; Pred. No. 2e-18;
Live 28; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogen regulatory protein P-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA
                                                                                                                                                                                                                                                          HSSP, P38504; IGNK.
InterPro; IPR002187; PII_GlnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
Pfam; PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Rd / KW20 / ATCC 51907;
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                            EMBL; X71659; CAA50650.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                             PIR; S33180; S3318C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                  EMBL; AF002994; BAS47945.1; -.
InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_glnB.UMP_S.
InterPro; IPR00343; PII_glnB.UMP_S.
PERM; PR00544; PII_glnB. 1.
PRINTS; PR00496; PII_glnB; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
Transcription regulation; Nitrogen fixation; Complete proteome.
BINDING 51 51 UMP (BY SIMILARITY).
GROTIFNCE 112 AA; 12200 MW; CF0F60FE7185465A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.7%; Pred. No. 3.1e-18;
Matches 51; Conservative 27; Mismatches 28; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 BIVVSKDQVEDVIEKIIBEARTGEIGDGKIFLLPVSDVIRVRIGERG 109
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Search completed: May 24, 2004, 19:13:35 Job time: 11.5 secs

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May 24, 2004, 19:09:38; Search time 36 Seconds
(without alignments)
990.377 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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sp_bhage:*
sp_plant:*
sp_rodent:*
sp_varus:*
sp_vartebrate:*
sp_unclassified:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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seq length: 200000000
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Maximum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9zst5 ricinus com	Cyzsta arabicopsis	Q9ari4 medicago sa	091422 anabaena sp	O9laq3 synechococc	Q8dla5 synechococc	Q9jwc4 neisseria m	Q9jxk6 neisseria m	Q7v5r4 prochloroco	Q8gqs4 acetobacter	Q7u8z7 synechococc	Q7va51 prochloroco	Q8kuj2 neisseria m	Q9ezq2 azoarcus sp	Q91400 prochloroco	Q7v025 prochloroco
SUMMARIES	מו	Q9ZST5	Q9ZST4	Q9ARI4	Q9L422	Q9LAQ3	Q8DLA5	Q9JWC4	99лжке	Q7V5R4	Q8GQS4	Q7U8Z7	07VA51	Q8KUJ2	Q9EZQ2	Q9L400	Q7V025
		10	10	10	16	~	16	16	16	16	ď	16	16	N	C1	7	76
	Duery Match Length DB	197	196	194	112	112	112	112	112	112	112	112	112	108	112	112	112
æ	Query Match	100.0	91.4	88.3	9.95	56.3	55.9	54.5	54.3	54.3	53.1	53.1	52.5	51.6	51.4	51.4	51.4
	Score	557	505	492	315.5	313.5	311.5	303.5	302.5	302.5	295.5	295.5	292.5	287.5	286.5	286.5	286.5
	Result No.	1	8	3	4	Ŋ	9	7	80	σn	10	Ħ	12	i el	4	15	16

Q7vpk6 haemophilus			Cluuzi rnodopireli		O8fp24 corynebacte	Q8ebj6 shewanella	_		O9kpx3 vibrio chol	Ogamm9 azospiritiu	Q7wji4 bordetella	O7wael bordetella	σ		P94125 azorhizobiu	Q8khs5 neisseria m	Q8kuj0 neisseria m							Q8kh45 neisseria m				P94852 herbaspiril
Q7VPK6			Q7UUZ1	Q8KUJ5	Q8FP24	QSEBJ6	031188	08ZC09	Q9KPX3	O9AMM9			Q7VVG9	P70731	P94125	QBKHS5	QBKUJO	Q9X705	Q8KI77	Q8KI 78	QBKUJ.	OBKUT3	Q8K158	Q8KH45	OBUEIB	QBKUIB	Q8KHB9	P94852
16	16	16	16	N	16	16	ď	16	• •	7	•	16	16	N	Ċ	N	Ċ	16	7	7	7	7	7	7	16	2	7	CI
112	114	114	133	105	112	112	112	112	114	112	112	112	112	112	112	101	101	112	100	100	86	9	99	100	157	98	6	113
51.3	50.9	50.7	50.7	50.5	50.2	50.2	50.0	50.0	49.8	49.6	49.5	49.5	49.5	48.9	48.9	48.7	48.6	48.6	48.4	48.4	48.2	48.2	48.2	48.2	4B.2	48.0	48.0	48.0
285.5	283.5	282.5	282.5	281.5	279.5	279.5	278.5	278.5	277.5	276.5	275.5	275.5	275.5	272.5	272.5	271.5	270.5	270.5	269.5	269.5	268.5	268.5	268.5	268.5	268.5	267.5	267.5	267.5
17	18	13	20	21	22	23	24	25	26	27	28	29	0.5	i H	32	3 6	3.4		9.6	3.7	e) (r	o e	40	41	4	43	44	4.5

#### ALIGNMENTS

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                                                                                                                                                                                                       SECURNCE FROM N.A.
MEDLINE=99030678; PubMed=9811909;
Hsieh M.H., Lam H.M., van de Loo F.J., Coruzzi G.;
"A PII-like protein in Arabidopsis: putative role in nitrogen sensing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 557; DB 10; Length 197; 100.0%; Pred. No. 2.3e-45; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 95:13965-13970(1998).

EMBL, AR095454, AAC78332.1; -.

HGSP, P05826, 2PII.

HGSP, P05826, 2PII.

GO; GO:0006808, P:regulation of nitrogen utilization; IEA.

GO; GO:0006808, P:regulation of nitrogen utilization; IEA.

Interpro; IRR002187; PII.glnB.

Pram, PR00549, P-III, 1.

PRINTS; PR00340; PIIGAIR.

ProDom, P0001194; PII.glnB; 1.

PROSITE; PS00638; PII.GlnB.CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     197 AA; 21781 MW; 2D18A50F15406B20 CRC64;
                                                  197 AA.
                         PRT;
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                         PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                  NCBI_TaxID=3988;
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SEQUENCE
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RESULT 1
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1 EYKVBAIIRPMRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV

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PII protein.
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09ARI4
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72 FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSBDKFVAKV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Spice L.A., Huang B.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
Mewes H.W., Lemcke K., Mayer K.F.K.;
                                                                                                                                                                                                                                               01-MAY-1999 (TEMBLrel. 10, Created)
01-MAY-1999 (TEMBLrel. 10, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
PII protein (P II nitrogen sensing protein GLB I) (At4g01900).
T7B11.6 OR AT4G01900.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NOBL TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Huang E.N., Nascimento L., de la Bastide M., Habermann K., Vil M.D.,
Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A.,
O'Shanghnessy A., Rodriguez M., Shekher M., Swaby I., Schutz K.,
Parnell L.D., Dedhia N.M., McCombie W.R.,
"Arabidopsis thaliana BAC 77811 from chromosome IV near 10 cM.";
Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                     KMEIVVSKDQVEDVIEKIIERARTGEIGDGKIFLLPVSDVIRVRIGERGDKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDMed=9811909; MEDMENE=9930678; PubMed=9811909; MESIED M.H., Lam H.M., van de Loo F.J., Coruzzi G.; MESIED M.H., Lam H.M., van de Loo F.J., Coruzzi G.; M.A. PII-like protein in Arabidopsis: putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; F:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_glnB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00638; PII_GLNB_CTER; 1.
SEQUENCE 196 AA; 21275 MW; PE740EA66776F157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensing.";
Proc. Natl. Acad. Sci. U.S.A. 95:13965-13970(1998)
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PRINTS; PR00340; PIIGLNB.
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                                                                                                1 FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago sativa (Alfalfa).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                         Gaps
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                                                                                                                                                                                                              Length 194;
                  Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia-Ibilcieta D., Sengupta-Gopalan C.;
"Characterization of PII (GLNB) in alfalfa.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Bubmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
HSSP, P38504; DAK16221.1; -.
HSSP, P38504; DAK.
GO; GO:0030234; F:enzyme regulator activity; JEA.
InterPro; IPRO02187; PII glnB.
PFem; PF00543; P-II; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.3%; Score 492; DB 10; Length 1
85.8%; Pred. No. 3.7e-39;
ive 8; Mismatches 8; Indels
Score 509; DB 10; Lengtu ...
Pred. No. 8.9e-41;
Pred. 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00340; PIIGLNB.
PRODOM; PD001194; PII glnB; 1.
PR0SITE; PS00638; PII GINB.CTER; 1.
PR0SITE; PS00638; PII GINB.CTER; 1.
SEQUENCE 194 AA; 21413 WW; 23FA623FF4D97450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PII protein (Nitrogen regulatory protein P-II).
Anahaman
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                           4; Mismatches
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Gonzalez L., Phalip V., Zhang C.C.;
                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                      91.4%;
90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrBMBLrel. 17,
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                                                                  Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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97; Conserva
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                         Query Match
Best Local Similarity
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112 AA; 12432 MW; C3F0AAS625E9F870 CRC64;
                                                                                                                                 60; Conservative
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                                                                                            Local Similarity
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SEQUENCE 112 AA
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QBDLAS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
      "Phosphorylation of the signal transduction protein PII by the Ser/Thr kinase PkrC in the cyanobacterium Anabaena sp. strain PCC 7120."; submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 EIVVSKDQVEDVIBKIIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 EIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRIRTGEKNTEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakamoto T., Gruber T., Bryant D.A.; "Nucleotide sequence of glnB and bcp genes in Synechococcus sp. PCC7002.";
                                                                                                                                                                MEDLINE=21595285; PubMed=11759840; Karitz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.2%; Pred. No. 1.4e-22;
Matches 64; Conservative 22; Mismatches 23; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO: GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_GlnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
Pfam; PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; AH2095; AH2095.
HSSP, P05826; ZPII.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:006608; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glnB.
InterPro; IPR002132; PII glnB. UMP.S.
PFam; PF00543; P-II: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA; 12492 MW; F74E54C38B67596B CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        cyanobacteřium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AJ251822; CAB75358.1; -.
EMBL; AP003589; BAB74018.1; -.
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PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PR00340; PIIGLNB.
PRODOM; PR001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                             1; Gaps
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BP-1;
MRDLINE=2225144; PubMed=12240834;
MRDLINE=22255144; PubMed=12240834;
MRDLINE=22255141; Faneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kobara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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  112;
                                                                                                                                                                                                                             63 ELVVSKDOVEDVIEKIIBEARIGEIGDGKIFLLPVSDVIRVRIGER 108
                                                                                                                                                                                                                                                          62 EIVIDDDQVDAVVDKIVAAARTGEIGDGKIFISPVDQIVKIRIGEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 9:123-130 (2002).

EMBL; AP005370; BAC08143.1; -..

EMBL; AP005370; BAC08143.1; -..

GO; GO:00030234; F:regulation of nitrogen utilization; IEA.

InterPro; IPR002187; PII glmB.

InterPro; IPR002332; PII_GlnB_UMP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 55.9%; Score 311.5; DB 16; Length C Similarity 58.2%; Pred. No. 3.5e-22; 64; Conservative 21; Mismatches 24; Indels
56.3%; Score 313.5; DB 2; Length 56.6%; Pred. No. 2.2e-22; tive 24; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Symechococcus elongatus (Thermosymechococcus elongatus) Bacteria; Cyanobacteria; Chrococcales; Symechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA; 12574 MW; 0248FDAE39505E06 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II 1.
GLNB OR NMA0447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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PRODOM; PROGNIB4; PII GINB; 1.
PROSTIE; PSOGG8; PII GINB CTER; 1.
PROSTIE; PSOG496; PII GINB_UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TIEMBLREL. 23, Create 01-MAR-2003 (TIEMBLREL. 23, Last s 01-OCT-2003 (TIEMBLREL. 25, Last s Nitrogen regulatory protein P-II. GLNB OR TLL0591.
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EMBL; AE002548; AAF42322.1;
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                            PIR; B81019; B81019.
HSSP; P05826; 2PII.
TIGR; NMB1995; -.
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Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 112 AA:
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STRAIN=MCS8 / Serogroup B;

STRAIN=201755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.P., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,

Nelson W.C., Gwinn M.L., Nahie O., Fleischmann R.D., Dougherty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                 DECISION AND A SERVING A SERVING A SERVING A STRAIN-22491 S. MEDLINE-2022556; PubMed=10761919; Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Riee S.R., Morelli G., Beham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Mitchead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EIVVSKDOVEDVIEKIIBEARTGEIGDGKIFLLPVSDVIRVRIGERGDKA 112
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Best Local Similarity 54.5%; Score 303.5; DB 16; Length 112;
Best Local Similarity 54.5%; Pred. No. 2e-21;
Matches 60; Conservative 25; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                          Bacteria; Proteobacteria; Betaproteobacteria; Meisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP S.
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01-0CT-2000 (TrBMBLrel. 15, Last sequence update)
01-0CT-2003 (TrBMBLrel. 25, Last annotation update)
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                     Neisseria meningitidis (serogroup A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD001194; PII gluB; 1.
PROSITE; PS00638; PII GLNB_CTER; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 404:502-506(2000).
EMBL, AL162753; CAB83744.1; -.
PIR, H81961; H81961.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00340; PIIGLNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002332; P. Pfam; PF00543; P-II; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningicidis Z2491."
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                                                                                                                 NCBI_TaxID=65699;
                                                                                                                                                                                            SEQUENCE FROM N.A.
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z. I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb B.A., Zhaer E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
GO, GG:0030234; F:enzyme regulator activity; IEA.
GO, GG:0006808; P:regulation of nitrogen utilization; IEA.
InterPro: IPR002187; PII_GlnB. UMP_S.
FIRST PR00343; PII; 1.
FRUNTS; PR00349; PII; 1.
PROSITE; PR00349; PII GlnB. UMP_S.
PROSITE; PS00638; PII_GlnB. I.
PROSITE; PS00638; PII_GlnB. I.
PROSITE; PS006496; PII_GLNB_UMP; 1.
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56.4%; Pred. No. 2.5e-21;
Live 19; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                            54.3%; Score 302.5; DB 16; Length
53.6%; Pred. No. 2.5e-21;
tive 26; Mismatches 24; Indels
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EMBL; BX572099; CAE21656.1; -.
Complete proteome.
SEQUENCE 112 AA; 12362 MW;
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NCBI_TaxID=1219;
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Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P., Palenik B., Regala W., Allen B.E., McCarren J., Paulsen I., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
EMBL; BX569690; CAE06977.1; -.
Complete proceome.
SEQUENCE 112 AA; 12340 MW; 387C54E0F85EEFD3 CRC64;
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                                                                                                              Acetobacter diazotrophicus (Gluconacetobacter diazotrophicus).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
NCBI_TaxID=33996;
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Perlova C., Meletzus D.;
Submirted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318039; AAN59757.1; -.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
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PROSTIE; PS00638; PII_GLNB CTER; 1.
PROSTIE; PS006396; PII_GLNB UTER; 1.
SEQUENCE 112 AA; 12431 WW; 52AB6F9C0CC8D124 CRC64;
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NCBI_TaxID=84588;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II.
                Created)
Last sequence update)
Last annotation update)
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Interpro; IPR002187; PII glub.
Dfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
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                  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                                  Regulatory protein PII.
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Q7U8Z7
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3 KVEAILRFWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
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X MEDLINE=22040572; PubMed=12045242;
MEDLINE=22040572; PubMed=12045242;
Comanducci M., Bambini S., Brunelli B., Adu-Bobie J., Arico B.,
Comanducci M., Giliani M.M., Masignani V., Santini L., Savino S.,
A Capecchi B., Giliani M.M., Masignani V., Santini L., Savino S.,
A Granoff D.M., Caugant D.A., Pizza M., Rappuoli R., Mora M.;
A Granoff D.M., Caugant D.A., Pizza M., Rappuoli R., Mora M.;
I. J. Exp. Med. 195:1445-1454(2002).
B R. Exp. Med. 195:1445-1454(2002).
B R. Exbl., AF452475; AAM53097.1; -..
GO; GO:0030234; F:enzyme regulation of nitrogen utilization; IEA.
R InterPro; IPR002332; PII glnb.
R InterPro; IPR002332; PII glnb.
R Pfam; PF00543; P-II; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Prochlorococcus marinus.
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II (Fragment).
Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
62 DVVVDJERVDDVVKAIADAARTGEIGDGKIFISSVDSVVRIRTGDRDSSA
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01-071-2003 (TrEMBLrel. 25, Last sequence update)
01-071-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein PII.
GLNK OR PRO1616.
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STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486;
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GlnB protein
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"Occurrence of three PII-like signal transmitter proteins in the diazotrophic proteobacterium Acoarcus sp. BH72.";
Wol. Microbiol. 38.276-288 (2000).
EMBL; AF281017; AAG40188.1;
HSSP; P05826; 2PII.
GC; GC:0030234; F:eazyme regulator activity; IEA.
GC; GC:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_GlnB_UMP_S.
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                                                                                     DB 2; Length 108;
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Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
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PROSITE; PS00438; PII_GLNB CTER; 1.
PROSITE; PS00496; PII_GLNB UMP; 1.
PROSITE; PS04496; 112 AA; 12273 WH; 636DBAF1909426A7 CRC64;
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                                                                                                                                                                                                                                                                                Q9EZQ2;
01-MRR-2001 (TrEMBLrel. 16, Created)
01-MRR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.4%; Score 286.5; DB 2;
48.2%; Pred. No. 8.5e-20;
tive 30; Mismatches 26;
                                                                                  51.6%; Score 287.5; DB 2;
52.8%; Pred. No. 6.5e-20;
iive 25; Mismatches 25;
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               PRODOM; PD001194; PII GINB; 1.
PROSITE, PS00638; PII GINB CTER; 1.
PROSITE; PS00496; PII GINB UMP; 1.
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MEDLINE=20521930; PubMed=11069654;
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NCBI_TaxID=62928;
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Q9L400 Q9L400; 01-OCT-2000 ( 01-OCT-2000 (

112 AA

PRELIMINARY;

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3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM 62
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          Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                   GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_GINB.
PENSTYS; PR00340; PIIGLNB.
PRODM; PD001194; PII_GINB.
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PROSTYE; PS00638; PII_GINB CTER; 1.
SRQUENCE 112 AA; 12314 MW; 42B3497E6B4472CD CRC64;
Prochlorococcus sp. (strain PCC 9511)
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May 27, 2004, 13:35:34; Search time 2414.89 Seconds (without alignments) 14663.718 Million cell updates/sec
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1 CTGAAAGTTGTGTTAAAAAA.....GTTCCTAATAAAAAAAA 817
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DEFINITION ACCESSION VERSION KEYWORDS

/trānslation="waasmykpisitsigfysdrknjafsdcisicsgfrhsrpscld lutkspsnnsrulpuvsaqissdyiddskfykvealvrpwriqqussallkigirgvt vsdvrgfgaqqsstrhqgsefsedkfvakvemelvvkkdqvesvintilegartgei gdgkifvlpvsdvIrvrtgergekaekmiqdmlsps" ò 242 240 362 360 422 420 482 480 122 182 180 GACTICGAAATTTTACAAGGTGGAAGCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCA 302 300 Arabidopsis thaliana Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Tosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 62 09 ATTIGITCIBGATTCAGACATTCCCGACCATCTTGCCTCGATTTGGTCACAGAAGTCACCG AGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAATATCTTCTGATTATATTTCCA TCGGCTTTACTGAAAATCGGGATTTCGAGGTGTTACTGTTTCTGATGTGAGAGGGTTTGGT GCACAAGGAGGTTCTACCGAGGAGACACGGTGGCTCTGAGTTCTCGGAAGACAAATTTGTT GCTAAAGTTAAGGATGGAAATCGTTGATAAGAAGACCAAGTGGAATCTGTAATCAACACA ATAACTICICICGGITICTAITCIGAICGAAAGAACAITGCITICICIGAITGCAITICG 241 GACTCGAARITITACAAGGTGGAAGCAATTGTCAGACCATGGAGAATCCACGAGTTTCA 301 resectivacreadaaressaarresassuratracrearsreadsassassurs GAAAGTTGTGTTAAAAAAAAAACTAGAATCATGGCGGCGTCAATGACGAAACCCATCTCA Gaps 1 (bases 1 to 844) Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G. A PII-like protein in Arabidopsis: putative role in nitrogen University, 100 , USA Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13965-13970 (1998) 99030678 .. nitrogen sensing" Length 844; Chases 1 to 844)
Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.:
Direct Submission
Submitted (29-SEP-1998) Biology, New York University
Washingron Square Bast, New York, NY 10003, USA
Location/Qualifiers 0; Indels 98.9%; Score 808; DB 8; Le 100.0%; Pred. No. 8.9e-182; ive 0; Mismatches 0; thaliana" /function="putative role in /note="GLB1" /codon\_start=1 /product="PII protein" /protein\_id="AAC78333.1" /db\_xref="GI:3885943" 1. .844 /organism="Arabidopsis /mol\_type="mRNA" /db\_xref="taxon:3702" /chromosome="IV" /map="10.8 cM" Conservative .621 al Similarity 808; Conserv 423 원 g ð

us-09-756-541-13.rge

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Unclassified.
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Coruzzi,G.M., Lam.H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-FII genes
L Patent: US 6177275-A 15 23-JAN-2001;
Location/Qualifiers
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patent US 6177275.
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AR125591 589 bp
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AR125591.1 GI:14111653
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                       Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
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/organism="Arabidopsis thaliana'
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                                                                                        /mol type="mRNA"
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/chromosome="4"
/clone="U23463"
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         Ecker, J.R.
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Coruzzi, G.M., Lam, H. M. and Heich, M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 16 23-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                  35.1%; Score 286.4; DB (69.8%; Pred. No. 1.3e-57;
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 14 23-JAN-2001;
Location/Qualifiers
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PLN 19-NOV-1998
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wiridiplantae; Streptophyta; Core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Acalypheae; Ricinus.
1 (Baese I to 840)
1 (Baese I to 840)
1 (Baese I to 840)
2 Plane I to 840)
3 Pli-like protein in Arabidopsis: putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
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                                                                                                                                                                                                                                                                                                                                                                                                                         244 CCCTGGCGAGTCTCGCAGTTCCTCGGCTTTGCTAAAAATTGGTATTCGAGGTGTTACT 303
                                                                                              39 GCGTCAATGACGAAACCCATCTCAATAACTTCTCGGGTTTCTATTCTGATCGAAAGAAC 98
                                                                                                                                               99
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                                                                                                                                            7 gaggciacnecgaaaktnesschingchechechertreathaaeareaasaaaa
                                                                                                                                                                                                99 ATTGCTTTCTCTGATTGCATTTGCTTTTGGATTCAGACATTCCCGACCATCTTGC
                                                                                                                                                                                                                              67 ILCCTGITTICATITICAGIIIGITICACCAAGCIIAAAAAITTCICAC
                                                                                                                                                                                                                                                                                                 159 CTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCC
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Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.M.
Hsiet, Submission
Submitted (29-SEP-1998) Biology, New York University, 100
Washington Square East, New York, NY 10003, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13965-13970 (1998)
99030678
                                                     'n
     Length 594;
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cds.
Score 285; DB 6; Length 59
Pred. No. 2.8e-57;
0; Mismatches 165; Indels
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partial
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120185 bp DNA linear PLN 01-APR-1999 complete sequence.
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/product=*PII protein"
/product=*PII protein"
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/db_xref=*G1:1377515"
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IFLIPVSDVIRIRTGERGEQAERMAGGITDALYV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AAAGITGAAGCCAITCICAGGCCAIGGAGAICCCICAGGIIICIICGGGIIIGIIGAAAA 273
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                                                                                     Unpublished

2 (Dases 1 to 796)

Garcia-Ibiloita,D. and Sengupta-Gopalan,C.

Direct Submission
Submitted (22-FEB-2001) Molecular Biology Program, New Mexico University, Corner of Knox and College, Las Cruces, NM 88003,
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                                                  Sengupta-Gopalan,C.
(GLNB) in alfalfa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.1%; Score 253.8; DB 8 71.0%; Pred. No. 7.3e-50;
                                                                                                                                                                                                                     /organism="Medicago sativa"
                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:3879"
1. .796
                                                                                                                                                                                    Location/Qualifiers
                                                  and
PII
                                                                                                                                                                                                                                                                                       'gene= "GLNB'
                                                                                                                                                                                                                                                                                                                       gene="GLMB"
                                    1 (bases 1 to 796)
Garcia-Ibilcieta, D.
Characterization of
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JOURNAL
                                                                                                      REFERENCE
AUTHORS
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                                       EFERENCE
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                                                                     TITLE
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                                                                                                                                                                                        /translation="HEATAKLGLLTPLHSNNIKKEFPVFDFSLFCPELRHSRFSHFNT AVKRVRYAPVVPVINAGSSPPYIPDAKFYKVEAILRPWRVSQVSSALLKIGIRGVTVS DVRGFGAQGGSTERQGSSEFSEDKFVAKVKMEIVVSKDQVEDVIEKIIBBARIGEIGD GKIFLLPVSDVIRVRTGERGDKAERMTGGRSDMSTSA"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Medicago sativa PII protein (GLNB) mRNA, complete cds.
AY027892
                                                                                               in nitrogen sensing"
                                                                                                                                                                                                                                                                                              Length 840;
                                                                                                                                                                                                                                                                                             34.9%; Score 285; DB 8; Length 84
70.3%; Pred. No. 2.7e-57;
live 0; Mismatches 165; Indels
                    1. .840
/organism="Ricinus communis"
                                                                                             /function="putative role
/note="GLB1"
                                                                                                                                              /product="PII protein"
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/db_xref="GI:3885941"
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/db_xref="taxon:3988"
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                                                                                                                                /codon_start=2
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Best Local Similarity
Watches 397; Conserv
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ACCESSION
VERSION
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SOURCE
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AY027892
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.11371,11559. .11770,11843. .12130,
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DIIRKOLVEKKAELADINKFRQTLIIRERRTYDELQEARKELVNCMGELVRKPFVDAM
QCKYCQEDVEDRAVEVLQLMEHYINDPDWHPYKRVKLENQOREVEVIDDRDEKLRELK
ADLGDGPYNAVTKALLBINEYNPSGRYITTELWNFKEDKRATLEBGVTCLLDQWEKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEOROHILKOSTESSESSYSSISDRPISLLSENGLILLILALUV
LLLGVILDPWEGSPLFIFPNRISSSLSPSPGSKWRDYTLAQARFVAROGTVIVCAVSS
PFIPELINWILSVSROKHODKYLVIBEDYITLYKNEKWPFRAFARHVILPPALDSKTAFSF
GSQGFPNFTARRPQHILQIIELGYRVWYNDDWWLQDPFLYLLGSBHAYFTPDMPQI
KPLMBSHDLPHPDRAGTYICSCMIYLRPTNGAKLLMKKWSEELQSQAWSESIRFKAN
DOPARNIAKKTAHQYDLYILSQVAPPTGGLYFKNEAWVQETKGKHVIVHNNYIIGYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/evidence=not_experimental
/produce="hypothetical protein"
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/db_xref="GI:4558547"
/tb xref="GI:4558547"
/translation="MGGTRHCYGLGYEMFNFVWSSSVRFVW8SSETLFKIVIITRSLC"
                                                                                                                                                                                       AF104919; similar to A. thaliana CHP-rich proteins encodes
by T10M13, GemBank accession number AF001308; functional
catalog ID=98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFVHKKCGDBASECTENPFHENHPLALGFLSRLQRQHWLKVYRSCDLGGKNIGDLFYR
CEICDFDMDLHCAKYPPLEVIDIPEMHSHKLNLLKDRVEFDCDAKGGKIGYGFPYECH
BCDSKFHVDCVRYSSSBEVGHPLEVNHSYHSLHPLXLLMGPPDYSDGKCRLGGRKID
DKLFYHGCSCNFTLDMRCVHPPPKSVLDLKTHDHQLNLLPRIFFFTCNACGLNGDRS
PYACFQCDFLITKOCPGLPRLININHDHRISRTSLIGIVUSVCGVCRQKVDMYCGGY
SCQRCSTYIAHSKCAREDVNNGKELEGVPEEIEDIEPYVVIDDNTIQHFSHKEHYMR
LAVNGLMCEVNKRCNACNHPISPQSFYGCMDCDFILHQNCAFPRRKWHVLHNERLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTSEVNI FGCSACHKI FUGFRYEHEDTKLDVLCGSFSEPFIHPSHPHPLYCLSPEDD
BVCSGCNBRSYHVLRCI EDNCGFILDFGCATFPQVVKHRI EDQPLSLCYGEKASGKYM
CDICKKETNDNTWFYTCKDHRASLHTWCVLGDFWGLI PKSTIELMNISYEVVLNNSIS
RPICRHCKSHCIPPIILKKIGTSDPYFCSLDCIESFRRLMRAK"
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LRDBYILRGLINNGLLFDKAYRVDGHGKKDMMKKDGPRLGLYGWIAGADDYNVDGREGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESAKLINA I QERTMRH I QKI VDDHERL TKLLESEKKKLE I KGNELAK PQVHNGTERMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDSDGVSVPLIHEHLMMPCNDLRRGDCCERLEAISDGYYCTTCD
   GenBank accession number AF104919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /_note="encodes hypothetical protein; identical to T15816.7, GenBank accession number AF104919; gene model last edited on 3 Mar 99"
/evidence=not experimental
join(10826. ..10842,10929. .11371,11559. .11770,11843. .1
/gene="T7811.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="encodes hypothetical protein; identical to
TISB16.8, GenBank accession number AF104919; gene model
last edited on 3 Mar 99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenBank accession number
functional catalog ID=99"
                                                                                                                                                                /note="identical to T15B16.6, GenBank accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
join(8080. .8568,9318. .9479,9557. .9778,9900. .10112)
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                                                                                                                                                                                                                                                                                                                         /evidence=not experimental
/product="putative CHP-rich zinc finger protein"
/protein_id="AAD22638.1"
identical to T15B16.6, GenBank acces
gene model last edited on 3 Mar 99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/evidence=not_experimental
/product="hypothetical_protein"
/protein_id="%AD22639.1"
/db_xref="GI:4558546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identical to Ti5B16.8, AF104919; similar to T7B11.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKMKRFQDYGLWLVDDHALESPLGKLE"
                                                                         /evidence=not_experimental complement (2647. .4650)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="GI:4558545"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="T7B11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="T7B11.3"
                                                                                                                                                                                                                                                                                                     codon start=1
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VCAVSSPFLPFLNNWLISVSRQKAQEKVLVIAEDYITLYKVNEKWPGHAVLIPPALDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTAYSFGSQGFFNFTARRPQHLLQILELGYNVMYNDVDMVWLQDPFQYLEGSHDAYFT
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IRFKANDQPAFNLALNKTAHQVDLYLLSQVAFPTGGLYFNDAAWVKETKGKHVIVHNN
YIIGYDRKMRRFQDYGLMLVDDHALESPLGKLQ"
                                                                                                                                                                                                                                                   1 (bases 1 to 120185)
Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K.,
Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A.,
Vil, M.D., Preston, R., Spiegel, L.A., Shekher, M., Swaby, I., Schutz, K.,
Parnell, L.D., Dedhia, N.N. and McCombie, W.R.
Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. (bases 1 to 120185)
Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Vil, M. D., Freston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A., Vil, M. D., Preston, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K., Parnell, L.D., Dedhia, N. M. and McCombie, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-MAR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724
3 (bases 1 to 120185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana BAC T7B11 from chromosome IV near 9.5 CM Trabidopsis thaliana BAC T7B11 is oriented toward the NOR and overlaps with T15B16, GenBank accession number AF104919. The SP6 end of T7B11 is occiented toward the centromere and overlaps with T10M13, GenBank accession number AF001308. There are no discrepancies found in these independently finished overlaps. The region from position 110064 to 110253 exists as single stranded and single chemistry. Please see the feature below for details.
                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/gene="T7B11.1"
/note="identical to 715B16.9, GenBank accession number
AF104919; similar to 77B11.3; functional catalog ID=99"
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/gene="T7B11.2"
/note="encodes putative CHP-rich zinc finger protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="overlap with T15B16, GenBank accession number AF104919, from position 1 to 14923" 50. .1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
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/produce=hypochetical protein"
/protein id="AAD22637.1"
/db_xref="G1:4558544"
                                                                                          Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/chromosome="IV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="near 10 cM"
1. .14923
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                       GI:4510323
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                                                                                                                           Arabidopsis
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AUTHORS
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JOURNAL
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COMMENT
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Direct Submission

Lybmitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bberc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV6 at the 3' end.
Location/Qualifiers
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RCLGTAVBAALAI I OGPSABGSRGVVRRAGGNSR I I VCAGGTT YGGEGSVPHSMSHPN
RCLGTAVBALAI I OGPSABGSRGVVRRAGGNSR I I VCAGGTT YGGEGSVPHSMSHPN
GRAPOVDLQRARAGSHGLLEVRCSDDI LI TQVI OFBEBABETHBIT KRIDALBDF
GRAPOVDLQRAATRAGSHGLLEVRCSDDI LI TQVI OFBEBABETHBIT KRIDALBDF
RLGSRAVILSRRTLLAKNQROMONDMENT TUDRI KIDI ALKEGSQVPKSKLY SF
YLGSVBERASANI I SRRTLLAKNQROMONDMENT TUDRI KIDI ALKEGSQVPKSKLY SF
FLGSSLPBLLPHIRROPLICNI I GHEDBRSVLRNILFLNASPDLSLRNVAPRCLINGGE
GGTFBELPAYDLSMQSDRAVILDHGTDVFINLGAELSADEVKSAAULAAEELT
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PRRPRAPTPGPPVRASPSSLLSPANGIRTGSPIPRLSPTPGPPVVRHTPVKPAAVP
PRTSPATPGPPGRAYSSANSSLPVSTPSPYSNGSSVGSQRDLPDVVRMEPIAADSPYU
PSATVLKQKCLANVASIGFORT 1VSAGREISPGPOIIQRDFRCLNCCAYSNPYSSII
IGSGQMCVTICRNMASKGRYVASSKNELQNFPELSLPLVDYVQTGNKRPGFVPASDS
RTSAPVYLVIDECLDBEPHLQHLQSSLHAFVDSLPQTTRIGIILYGRYVSIYDFSEDSV
                                                                                                                                                                    PLN 16-MAR-2000
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Spiegel, L.A., Huang, E.N., Nascimento, L.U., de la Bastide, M., Vil, D.M., Preston, R.R., Matero, A., Shah, R., C'Shaughnessy, A., Rodriguez, M., Shekher, M., Schutz, K., See, L.H., Swaby, I., Habermann, K., Dedhia, N.N., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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contains EST gb:H36218, AA651596, T42768, AI997386.1,
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/protein id="CAB80674.1"
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/db.zref="SPTREMBL:09SY11"
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/variety="Columbia"
/db_xref="taxon:3702"
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ioin(13384. .13454,13566. .13613,13697. .13757,13842. .13940,
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QVPRFLGLKVGLIQONTPRQNRTBCRTLNAILPATLNALSGRGVHVYTVNDYLARRDCEWVG
QVPRFLGLKVGLIQONTPRQRKGNYLCDITVVTNSELGFDYLRDNLATESVBELVLR
TVLTLTRQGYEDABRILDDVDLYDPREWSPRYSYVLNAIKAAFREDIHTTVDERQX
TVLTLTRQGYEDABRILDDVDLYDPREWSPRYSYVLNAIKARELFLRDNYJITARKSTLI
DEFTGRVWQGRRWRSOGLHQAVGRAREGLDIQNESITLASISYQNFPLQFPKLCGNTGTA
STESNAFFESIYKLKVTIVPTNRPMIRRDESDVVFKANNGKNRAVVEISRNHRTGRAV
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SKLSNVNSLPEKIMLKKQIAIGINEVTRVLERMNPNNTSDQQQNPKQLQVVILVADCK
PRMLTKHIPNLAASRNVPVLYVRDNKRASIRLGBLVKLKTALAIGIKARGNDLNLLK
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product="putative SecA-type chloroplast protein transport
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                                                                          note="encodes RNaseP-associated protein; identical to r15B16.20, GenBank accession number AF104919; gene model
                                                                                                                                                                                                                                                                                                                                             /note="identical to T15B16.20, GenBank accession number AF104919; functional catalog ID=98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="putative RNaseP-associated protein"
protein id="AAD22641.1"
db_xref="GI:4558548"
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/db_xref="GI:4558549"
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//gene="A4401830"
complement(join14552. .14905,14994. .15290,15475. .15738,
15809. .16075,16311. .17110,17180. .17979,18068. .18306,
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                .10501)
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/gene="AT4g01820"
/number=4
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/gene="AT4901820"
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/gene="AT4g01820"
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/gene="AT4g01820"
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/gene="AT4g01820"
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/gene="AT4g01820"
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/gene="AT4g01820"
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TVASFTGEKQAMKSYREFINLAYRASVKQGFSMGLGGUVPEVPFECSYALAIMFGEM

ILKKGYTGGEVVNWATVVASSARSLGQTTPCLIAFAAGKAAAYKMFETIERKPSIDAF

ILKGGYTGGEVNNWATVVASSARSLGQTTPCLIAFAAGKAAALVMEETIERKPSIDAF

DIAGKVLEDIRGEIELRADVCFSYPAREMEEVFGGFSLLI PSGAYAALVGESGGSGKSSV

SLIERFYDPSSGSVLIDGVNLKEFQLKWIRGKIGLVSQEPVLFSSSIMENIGYGKEN

ATVBEIQAAKLANAANFIDKLIPRCHETIGTOGREGGQKQRIAIARALKUPPRIL

ILDEATSALDARSERVVQERLDFRGHETIVGERGGGGQKRIAIARALKUPPRIL

ILDEATSALDARSERVVQERLDFRANKENITYARALNKPETTLI LIGTILGANOTIF PET FGIL

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FAXVIERFYGWPIDPENSGSTIGSRLASADALIKTIVGDSLSLSVKNAAAASGILI

AFTASWKLAVIIVMIPLIGINGYLQIKFIKGFTADAKAKYERSSQVANDAAGSIRTV
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SGLVLENVKGDIELALTWTAIGISQASSTAPDSSKAKGAAASIFGIIDGKSMIDSRDE
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ASEAEIIAAAELANAHGFISSIQQGYDTVVGERGIQLSGGQXQRVAIRKAIYKEPKIL
LLDBATSALDARSERVVQDALDRVWNRTTVVVAHRLSTIKNADVIAVVRGVIVEKG
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LFGDLIDSIGONOSNKDIVEIVSKVCLKFVYLGLGTLGAAFLQVACWMITGBRQAARI
RSLYLKTIILRQDIGFPDVETSTGEVVGRMSGDTVLILBAMGEKVGKFIQLIATFVGGF
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EFRFPAPRILAFKEARFPQIRTLTTEQRMKLKSSFIEFDEASFCEWMRSLKVVPPEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join 19603. .9956,10053. ,10349,10502. .10765, 10835. .11101,11218. .12029,12106. .12905,12987. .13225, 13293. .13514,13592. .13767,13850. .13904,13995. .14198))
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contains EST gb:A1996312.1, A1995010.1, A1994333.1,
R90081, AA605450"
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/gene="AI4g01820"
complement (join(9603. .9956,10053. .10349,10502.
10035. .11101,11218. .12029,12106. .12905,12997.
13293. .13514,13592. .13767,13850. .13904,13995.
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/product="P-glycoprotein-like protein pgp3"
/protein_id="CABB0675.1"
/db_xref="G1:126856"
/db_xref="G0A:Q9SY12"
/db_xref="SPTREMBI:Q9SY12"
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/gene="AT4g01820"
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/gene="AT4g01820"
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/gene="AT4g01820"
                                       complement(5603..5740)
/gene="AT4g01810"
/number=1
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/numher-^
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                                                                                                    complement (5741, .6061)
/gene="AT4g01810"
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/gene="AT4g01810"
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272 TGTCAGACCATGGAGAATCCAGGAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGG 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Tracheophyta;
Pinus; Pinus.
                                       418 TGAAGACACGITIGITGCAAAAGTTAAAATGAAATTGTTGTCAGCAAAGACCAGGTTGA 477
                                                                                                                                                                           538 ATTCTTGACTCCCATCTCCGATGTTATAAGAGTTCGCACTGGTGAACGGGGGAAAAAGGC 597
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Spermatophyta, Coniferopsida, Coniferales, Pinaceae,
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Pinus pinaster mRNA for PII-like protein (glb gene).
AJ489604
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/function="putative nitrogen
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/organism="Pinus pinaster"
/mol type="mRNA"
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/db_xref="GI:37653227"
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glb gene; PII-like protein.
Pinus pinaster
Pinus pinaster
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42. .773
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Direct Submission
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AUTHORS
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/db_xref="G1:38231570"
/tanslat-ion="MASPSISKSNFSLHSFSSSPSLSQPPHFTSITVVQPKFPPSQLT
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VRGPGAQGGLTERQAGSEFSEDTFVAKVYGME:VVSKDQVEGVIAKIIEEARTGEIGDG
                                                                                   52344
                                                                                                                                                                                                       947 bp mRNA linear PLN 15-NOV-2003
Lycopersicon esculentum PII-like protein (GLB1) mRNA, complete cds.
AY442185
AY442185.1 GI:38231569
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Subaryophyta; Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
Theses ito 947)
The complete in the complete in the complete in the protein in toward on Wiren, N.
A PII-like protein in toward
                                                    804
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Submitted (17-OCT-2003) Institute of Plant Nutrition, Hohenheim
University, Fruwirthstr.20, Stuttgart 70593, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCACAAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAATATC
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TAATAATGAATGGAGTCTGTGTTTGGTTTCATGTAATCGATCAATGTGTTTTTAAC
                                                                     52285 TGTACATCAATTATGCAGAAACATCTGTCCTGGTTCTCAGACATCGAAACTCTGTTCCTA
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Pred. No. 8.9e-48;
0; Mismatches 120; Indels
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Walch-Liu, P., Roemheld, V. and von Wiren, N.
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/product="PII-like_protein"
                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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VERSION
KEYWORDS
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AUTHORS
TITLE
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URE: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
Full Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Ryimura,T., Ikeda,K., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Matsubara,K. and Murakami,K., Sugano,S.,
Sugiyama,A., Matsubara,K. and Murakami,K., Genome Exploration Research Group in Riken Genome Sciences Center
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carinoi,P., Pukuda,S., Hanagaki,T.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imctani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kojima,Y., Kondo,S., Konno,H., Kawai,J.,
Itoh,M., Kagawa,I., Kojima,Y., Kondo,S., Konno,H., Kawai,J.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osaro,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACHATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGATTTTTGTTTTGCCT 539
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                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-DBC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Tarkehashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 ATTGATAAAGTTAAGATGGAAATAGTGGTGTCCAAGGATCAGGTTGAAGCTGTTGATC
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/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) cDNA clone:J013149B08, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKG68407.1 GI:32978425
FII CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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유 ð g ACCESSION VERSION KEYWORDS SOURCE REFERENCE

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Anamauncu, r., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Tida, Y., Kodama, T., Kurosaki, T., Kusumegi, T., Lul, M., Masua, J., Kodama, T., Kurosaki, T., Kusumegi, T., Lul, M., Mara, J., Mira, M., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Oka M., Kyu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Koshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, P., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Haramacto, T., Lakawa, T., Carninoi, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Haramoto, K., Itoh, W., Kagawa, I., Kangawa, S., Karch, H., Kawai, J., Kanda, I., Kangawa, S., Karch, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Shinagawa, A., Shiraki, T., Salco, K., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y. Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
                                                                                                                                            URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,P.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 GTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAAC 479
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
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/cultivar="Nipponbare"
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Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Carminci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hayatsu, N., Biramoto, K., Hiraoka, T., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Bashido, K., Hiraoka, T., Horta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishibiki, J., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kaituha, S., Kishikawa, T., Kojima, Y., Miura, J., Hiyazaki, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, M., Sano, H., Sasaki, D., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Sataki, P., Sagabo, Y., Sugano, S., Shiragawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayama, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Vanish, M., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kinchi, S., Satoch,K., Nagata,T., Kawagashiza,N., Doi,K., Kishimoto,N., Yazaki,J., Ishiskawa,M., Yamada,H., Ooka,H., Hutta,I., Kojima,K., Namiki,T., Onneda,E., Yahagi,W., Suzuki,K., Li,C., Chtsuki,K., Shinki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Kurosaki,T., Kodama,T., Maruda,H., Kobayashi,M., Xie,Q., Lu,M., Narikwa,R., Suguyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,U., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayateu,N., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Rondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Vochio, M., Matsubata,K., Shinagawa,R., Shiraki,T., Vochio, M., Matsubata,K., Shinagawa,R., Shiraki,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKUYY152 902 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023070H02, full
insert sequence.
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondal, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp,
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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AUTHORS
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Run on:

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Seguence:

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3373863 seqs, 2124099041 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

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#### SUMMARIES

8.4         349980         5         AAH68531         Aah68531         C glutami           8.2         1164         5         AAS88441         Aas88441 DNA encod           8.2         1106         4         AAS46256         Aas46256 DNA encod

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64.6	64.6	64.6	19	60.4	60.4	60.4	59.6	57.6	52.4	50.8	49.6	49.6	4	45.8	44.4	43.6	43.4	43.4	43.4	43.4	42.8
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### ALIGNMENTS

Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; ss. Arabidopsis thaliana P-PII cDNA. 96US-0022328P. 97US-00899330. Hsieh M; AAF58581 standard; cDNA; 817 (UYNY ) UNIV NEW YORK STATE. (first entry) Arabidopsis thaliana. Cornzzi GM, Lam H, WPI; 2001-158572/16 US6177275-B1. 24-JUL-1996; 23-JUL-1997; 23 - JAN-2001. 23-APR-2001 AAF58581; AAF58581 ID AAFE RESULT 1 

P-PSDB; AAB69495.

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 2; Fig 12; 35pp; English.

The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII mucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

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Arabidopsis thaliana; plant; gene; stress; transgenic;

Arabidopsis thaliana

WO200216655-A2 28-FEB-2002

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               Score 817; DB 4; Length 817; Pred. No. 3.8e-220; 0; Mismatches 0; Indels
250 T; 0 U; 0 Other;
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.

Zhu T;

WPI; 2002-304127/34.

(SYGN ) SYNGENTA PARTICIPATIONS AG Harper JF, Kreps J, Wang X,

(SCRI ) SCRIPPS RES INST

24-AUG-2000; 2000US-0227866P. 26-JAN-2001; 2001US-0264647P. 22-JUN-2001; 2001US-0300111P.

24-AUG-2001; 2001WO-US026685.

Claim 144; SEQ ID NO 2133; 577pp + Sequence Listing; English

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliama stress regulated gene (ABA111956-AB217574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the Buropean Patent Office
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Arabidopsis thaliana stress regulated gene SEQ ID NO 2133.

(first entry)

21-JAN-2003

XEXEXEX

ABZ14328

ВP

ABZ14328 standard; DNA; 591

ABZ14328 RESULT

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us-09-756-541-13.rng

OY 153 TCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTTTTTACCTGTCGTT 212  Db 121 TCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTTTTTACCTGTCGTT 180  C) 213 AGTGCCCAAATATCTTCTGATTATTCCAGAATTTTACAAGTGAAAGCAATT 272  Db 181 AGTGCCCAAATATCTTCTGATTATTCCAGAATTTTACAAGGTGGAAGCAATT 240  C) 273 GTCAGACCATGAGAATCTTCTGAATTATTCCAGAATTTTACAAGGTGGAAACAATT 240  C) 273 GTCAGACCATGAGAATCTACAGAAGTTTCATGGGCTTTACTGAAAATCGGAGTTTCAGAGT 330  241 GTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGGATTCGAGGT 3300	Qy         333 GTTACTGTTTCTGATGTGAGAGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACCACGGT         392           Db         301 GTTACTGTTTCTGATGAGAGGTTTTGGTGCACAAGGAGTTCTACCGAGAGACACGGT         360           Cy         393 GGCTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAG         452           Db         361 GGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTTAAAGTTAAGATGGTAATTGTTAAG         452	Qy         453 AAAGACCAAGTGGAATTCTGTAATCAACAATAATTGAAGGGCAAGGACAAGGAGAGATT 512           Db         421 AAAGACCAAGTGGAATCTGTAATCAACAATAATTGAAGGAGAAAGGACAAGGACAAGGATT 480           Qy         513 GGTGATGGCAAGATTTTGCTTTTGCTTAATGATGTCATAAGAGTTAGGACAGGTGAG 572           Db         481 GGTGATGGCAAGATTTTGTTTTTCCTTGTCAATGTCATAAGAGTTAGGACAGGTGAG 540		RESULT 4. AAF58582 XX	Ricinus communis P-E Castor bean; PII; pl nitrogen assimilatic Ricinus communis.	EX	
AAAGACCAACTGGAATCTGTAATCAACAATAATTGAAGGACCAAGGACAGGAGAGATT       512       Qy         AAAGACCAAGTGGAATCTGTAACAATAATTGAAGGACCAGGAGGATT       480       Db         GGTGATGGCAAGATTTTTGCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAG       572       Qy         GGTGATGGCAAGATTTTTGTTTTGCTGTGTCAGATGTTCATAAGAGTTAGGACAGGTGAG       540       Db         GGTGATGGCAAGATTTTTGTTTTGTTTTGTTTTGTTTTAGGTTTCACGGTCTTAG       540       Db         CGTGGGGAAGAATGATTTCACGTCTTTCACCGTCTTTAG       623       Qy         CGTGGGGAAAAAGAAGAAGAAGATGACTTCACCGTCTTAG       591       Db	andard; cDNA; 588 BP.	23-APR-2001 (first entry)  Arabidopsis thaliana P-PII cDNA fragment.  Dharabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII;  Arabidopsis thaliana.  Dharabidopsis thaliana.  Dharabidopsis thaliana.	00899330.	; 96US-0022328P. V NEW YORK STATE. Lam H, Hsieh M;	WPI; 2001-158572/16. P-ESDB; AAB69495. XX Novel P-PII genes capable of regulating plant nitrogen assimilation, Useful for transgenic plant production, and as probes for isolating XM additional genomic clones having P-PII gene promoters. XX Claim 2; Col 37-38; 35pp; English.	a nitrogen regulatory PII protein. Novel nucleotide sequences have been isolated.  g nitrogen assimilation in plants, and in They are also used to engineer organisms two screening of herbicides. P-PII obes for isolating additional genomic clones enes. P-PII promoters are light- and/or itable for genetic engineering of plants  7. 147 G; 172 T; 0 U; 0 Other;  Score 588; DB 4; Length 588;	0, Gaps '0;  TTCTGATCGA 92  [           TTCCCGACCA 152             TTCCCGACCA 120

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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                      Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 594 BP; 149 A; 117 C; 157 G; 171 T; 0 U; 0 Other;
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             96US-002232BP.
                                             (UYNY ) UNIV NEW YORK STATE
                                                                                     Lam H,
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                                                                                                                                          P-PSDB; AAB69496.
               24-JUL-1996;
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that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII contectives may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                                                                                                                             DB 4; Length 897;
                                                                                                         Sequence 897 BP; 254 A; 171 C; 218 G; 254 T; 0 U; 0 Other;
                                                                                                                                        Score 286.4; DB 4; Length
Pred. No. 2.3e-70;
0; Mismatches 171; Indels
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                                                                                            GCGTCAATGACGAAACCCATCTCAATAACTTCTCTCGGTTTCTATTCTGATCGAAAGAAC
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                                                 Gaps
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Ouery Match

34.9%; Score 285; DB 4; Length 594;
Best Local Similarity 70.3%; Pred. No. 4.7e-70;
Matches 397; Conservative 0; Mismatches 165; Indels
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Castor bean, PII, plant nitrogen regulatory gene, P-PII; nitrogen assimilation; transgenic plant, herbicide screening;

Ricinus communis

JS6177275-B1

97US-00899330

23-JUL-1997;

Ricinus communis P-PII cDNA fragment.

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vaccine, plant biocontrol agent
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P-PSDB; ADA34150.
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                                                                                                          ADA30024 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as ottis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 GCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 CGAGGIGITACIGITICIGAIGIGAGGITIGGIGCACAAGGAGGITCIACCGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13130 TGTCGTGATGATGGTTCATTCAATTATTGAGTCAATCATTAAAGTTGCAAATACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 GAGATTGGTGATGGCAAGATTTTTGCTTTTGCCTGTCAGAGGTGAGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 GITAAGAAAGACCAAGIGGAAICIGIAAICAACACACAATAATIGAAGGAGCAAGGACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 CACGGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTT
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                                                                                                                                                                                                   bronchopulmonary; endocarditis; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 345-368; 545pp; English
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                                      AAF28548 standard; DNA; 96109 BP
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                                                                                                                                                                                                                                                                                                                                               16-JUN-2000; 2000WO-US016649.
                                                                                                                                                                                                                                                                                                                                                                                99US-014C121P.
                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson C,
                                                                                                                                                                                                                                        Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                 Genomic fragment #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-041427/05.
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                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                            04-APR-2001
                                                                                                                                                                                                                                                                                                            28-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lagace RE,
                                                                           AAF28548;
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Matches
       RESULT 6
AAF28548
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267 GCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnossing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 caacecarracceracreaacrraaacerrarecercacaaacearacacara
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                                                                                   gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            رب
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DNA encoding Acinetobacter baumannii protein #1311.
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Pred. No. 6.5e-14;
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AAV2120 AAV212	Db 13284 TAAGGGTAGGGGAGTTCAAGGTTGAGAGGGTATAGGGGGAAGAGAGAG	of 57} of ACF67367 fr t into 57 fragments I Name Begin En 01 100001 21 02 200001 31 03 300001 41 04 400001 51 05 600001 71 06 600001 71 07 700001 81 08 900001 101	ACP67367
Color   Colo	AAV21209_11   100001 AAV21209 12   1200001 AAV21209 14   1400001 AAV21209 15   1500001 AAV21209 15   1600001 AAV21209 16   1600001 Duery Match 10.4%; 6 Sest Local Similarity 56.0%; 6 Atches 181, Conservative 0 249 AAATTTACAAGGGGAAGGO		

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39118 drańccecacedenekacaesarekacaesecearrraaciraarrreaarringaeser 89177
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                                                                                                                                                                                                                                                                                                                                                                556 GAGTIAGGACAGGTGAGCGIGGGGAAGAAGCAGAGAAGAIGATGATGATAIGCTITCAC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                            496 CAAGGACAGGAGATTGGTGATGCAGATTTTTGTTTTGCTGTCAGATGTCATAA
                                                                                           256 ACAAGGIGGAAGCAATIGICAGACCAIGGAAICCAGCAAGITITCAICGGCITIACIGA
                                                                                                                     88821 AAAGATTGATGCGATTATCAAACCTTTCAAATTAGATGATGTGCGTGAAGCTCTGGCGG
                                                                                                                                                                          88881 AAGTGGGTATCACCGGAATGACAGTAACAGAGGTGAAAGGTTTTGGGCGCCCAAAAAGGTC
                                                                                                                                                                                                                                 88941 ATACAGAGCTGTATCGCGGTGCAGAATATATGGTGGAT---TTTCTGCCAAAAGTGAAAA
                                                                                                                                                                                                                                                         TGGAAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAG
                                                                                                                                                 316 AAATCGGGATTCGAGGTGTTACTGTTTCTGATGTGAGGGGTTTGGTGCACAAGGAGGTT
                                                                                                                                                                                                     376 CTACCGAGAGACACGGTGGCTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGA
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                                      Length 110000;
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                                                     Pred. No. 1.1e-11;
0; Mismatches 179;
                                       ; DB 7;
1.1e-11;
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                                       Score 81.6;
Pred. No. 1.
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696798
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(CNRS ) CNRS CENT NAT RECH SCI
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                                       10.0%;
52.6%;
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 500001
600001
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                                                                   202; Conservative
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                                                     Similarity
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  ACF65387 5
ACF65387 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACF72027;
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                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAGATTGATGCGATTATCAAACCTTTCAAATTAGATGATGTGCGGGAAGCTCTGGCGG 49366
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Pred. No. 1.1e-11;
0; Mismatches 179; Indels 3;
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tes 202; Conservative
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ACF67367_43
ACF67367_43
ACF67367_44
ACF67367_46
ACF67367_46
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ACF67367_50
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ACE67367 30
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ACF67367_39
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ACF67367_41
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ACF67367_48
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Continuation
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                                                                                                                                                                                                                                                                                                                                                                                                                   64039 ATACAGAACTTTATCGTGGTGCGGAATATATGGTGGAT---TTTCTGCCGAAAGTGAAAT
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                                                                                                                        Length 110000;
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Pred. No. 3.5e-11;
0; Mismatches 147; Indels
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3 LOCUS AAT42063 Accession Aat42063
                   The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of F. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of F. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. creombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence that process and feasures for which P. therefore an interval and diseases for which P. therefore and the proteins are as virulence that process and feasures for which P. therefore and the proteins are as virulence that the process and feasures for which P. therefore and the proteins are as virulence that the process and feasures for which P. therefore and the proteins are as virulence that the process and feasures for which P. therefore the process and the process and the process of the paragets of human diseases for which P.
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                                                                                                                                                                                                                                                                                                                                                                                                                            luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
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                                                                                                                                                                                                                                                              AAATCGGGATTCGAGGTGTTACTGTTTCTGATGTGAGGGGTTTGGTGCACAAGGAGGTT 375
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individuations of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records AB237706-ABZ42016 represent nucleic acid molecules of the invention
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Ratti G, Scarselli M,
                                                                                                                             Score 77; DB 7; Length 363;
Pred. No. 1.9e-11;
0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitidis partial DNA sequence gnm_20 SEQ ID NO:20.
                                                                                                Sequence 363 BP; 84 A; 77 C; 123 G; 79 T; 0 U; © Other;
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C, Mora M,
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Best Local Similarity 54.1%;
Matches 180; Conservative
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Rappuoli R, Pizza M;
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA25603 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81260 to AAA81201 and AAB25603 represent Neisseria DNA sequences; and AAA8122 to AAA8125 and AAA81212 to AAA8125 and Neisseria meningitidis DNA sequences; and AAA8122 to AAA81452 represent Neisseria meningitidis MenB polymucleotide ORF sequences, which are all need in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a medicament for treating, concenting or diagnosition. The composition can be used as a medicament for in the manufacture of a medicament for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identification of sequences from the bacterium will also facilitate production of sequences from the bacterium will also facilitate production of sequences from the bacterium will also facilitate production of hological probes, particularly corganism-specific probes. Attempts to make efficacious Meningococcus B vaccines have also been tried but none have successfully overcome artigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins char may be presumed targets for the immune system and which are not autigenically variable or at least more conserved than other more
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[bases I to 566]  Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M. Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatenu,M., Hayashizaki,J. and Shinozaki,K. and Shinozaki,K. Ingublished (2002) Unpublished (2002) Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-4960	OKGA	E ST	Euka Sper	ryota; matoph ds: eu	s thai Virid: Yta; Ma rosids	ipla:	ntae; Strept liophyta; eu Brassicales	ophyta; Embr ficotyledons ; Brassicace	hyta; Tr ore eudi Arabido	ophyta; ;;
and Shinozaki, K. Large scale analysis of Arabidopsis full-length cDNA Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002) Contact: Motoaki Seki Contact: Motoaki Seki Plant Functional Genomics Research Group RIKBN Genomic Sciences Center 3-1-1 Koydaai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 181-298-36-9060 Fax: 181-298-36-9060	REFEREI AUTH(	NCE	Seki Oono Arak	bases ,M., N ,Y., S	1 to 50 arusaka akurai, Shiba	66) a,M. T.,	, Ishida,J., Carninci,P.	Kamiya, A., Kawai, J.,	ou, M., Nakaj sh, M., Ishii, L, M., Hayashi	ma,M aki,]
Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Tel: 81-298-36-4359 Fax: 81-298-36-498-96-9060	TITE		and Larg Unpu	Shinoz e scal blishe	aki,K. e analy d (2003	ysis 2)	of Arabidop	sis full-len	CDNA	Z.
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and KhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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1. .566
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CB261070 549 bp mRNA linear EST 06-NOV-2003 33-E9570-012-004-A09-77R MPIZ-ADIS-012 Arabidopsis thaliana CDNA

clone MPIZp769A094Q 5-PRIME, mRNA sequence.

Arabidopsis thaliana (thale cress)

GI:32885843

CB261070.1

CB261070 EST

LOCUS ACCESSION VERSION KEYWORDS SCURCE

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/organism="Arabidopsis thaliana"
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/lab_mwpIZ-AlG-012"
/note="vector: pSPORTI; Site I: Sall; Site 2: NotI; cDNA
library from Arabidopsis thaliana, accession landsberg
erecta; six weeke old total plants were treated for 24
hours with different stresses, (1) at 4M-C in the dark,
(2), at 37 Grad C in the dark, (3) lying in the lab after
removing from soil, (4) in the greenhouse after wounding
leaves with a foreceps, (5) in the lab watering with a 150
mW NaCl solution, (6) at 26 Grad C in the light/UV; equal
quantities of stressed plant material were pooled; library
was made at the Max-Planck-Institute for Plant Breeding
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T7-Sall-CCACGCGTCG-Sprime-CDNA-DOlyA-CC-NOII-SP6; Note:
T7-Sall-CCACGCGTCG-Sprime-CDNA-DOlyA-CC-NOII-SP6; Note:
Sequencing granted in the context of the GBBI Arabidopsis
Verbund I: Genetic Diversity, 'Establishment of migh-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection,' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD, context RZPD (clone@rzpd.de) for further
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

1 (Dases I to 549)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weissbaar,B.
Large-scale identification and analysis of genome-wide single-runcheotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
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97.6%; Pred. No. 8.6e-94;
ive 0; Mismatches 11.
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Insert Length: 549 Std Brror: 0.00
Plate: 4 row: A column: 09
Seq primer: T7R; CTAATACGACTCACTATAGGGA.
Location/Qualifiers
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CD820903 732 bp mRNA linear EST 10-JUL-2003
BN25.040D05F011026 BN25 Brassica napus CDNA clone BN25040D05, mRNA
sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermacophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.

Genoplante.
                                                                                                                                               AGCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGAT 325
                             125 CCCACCGICTICCCTCGATTIGGICGCAAAACCACCGACCAAGGCTCGGGTTTCCCA 184
                                                                                                                                                                       TCGAGGTGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAG 385
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Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 AGGTGAGCGTCCCGGAGAAAGCAGAAGATGACTGGTGATATGCTTTCACCGTCTTAGGA
CCGACCATCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACC
                                                                                                                                                                                                                                                                                                                                                                           TGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGG
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                                                                                                           185 reregitadadececaaagererrargarrararriceagaereaaagriftacaagidda
                                                                                                                                                                                                                                               TGTCGTTAGTGCCCCAAATATCTTCTGATTATTCCAGACTCGAAATTTTACAAGGTGGA
                                                                                                                                                                                                                                                                                                   386 ACACGGTGGCTCTCACTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAAATCGT
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica napus"
/mol type="mRNA"
/cultivar="Jet neuf"
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/clone="BN25040D05"
/tissue_type="seed"
/clone_lib="BN25"
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CD820903.1 GI:32502843
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BN25;060G17F011129 BN25 Brassica napus cDNA clone BN25060G17, mRNA
sequence.
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Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                             432
                                                                                                                                                                                                                                                                                                                                        AGATGGAAATCGTTGAAAAAAAACACCAAGTGGAATCTGTAATCAACAATAATTGATG 489
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                                                                                                                                                                                 TGAAAATCGGGATTCGAGGTGTTACTGTTTCTGATGTTCGAGGGTTTGCTGCACAAAGAGAG
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                         TITACAAGGIGGAAGCAAITGICAGACCAIGGAGAAICCAGCAAGIIICAICGGCIITAC 312
                                                                                             TITACAAGGIGGAAGCAATIGTCAGACCAIGGAGAAICCAGCAGTITCAICGGCTITAC 309
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     TOGIGITITACCIGICGITAGIGCCCAAAIAICIICIGAITAIAIICCAGACIC-GAAAI 252
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Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Unpublished (2003)
Contact: Genoplante
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                                                                                                                                                                                                                                                                                                       AGATGGAAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAG
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                                                                                                                                                                                                                             GITCTACCGAGAGACACGGTGGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTA
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85.9%; Pred. No. 9.5e-86;
ive 0; Mismatches 84; Indels
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/cultivar="Jet neuf"
/db_xref="Laxon:3708"
/clone="NB5060G17"
/tissue_type="seed"
/clone_lib="BN25"
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CD825321.1 GI:32507261
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                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
Location/Qualifiers
1. 745
/organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGACCATCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.9%; Score 456.8; DB 14; B2.0%; Pred. No. 3.5e-85; ive 0; Mismatches 117;
                                                                                                                                                                                                                                                                                       /mol type="mRNA"
/cultivar="Jet neuf"
/db xref="taxom:3708"
/clone="BN2047L06"
/tissue type="seed"
/clone lib="BN20"
                    Contact: Genoplante
Genoplante
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Unpublished (2003)
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AGCAATTGTCAGGCCATGGAGAATCCAGCATGTTTCATCGGCTTTACTGAAAATTGGGAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGAGGTGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGAGGTGTAGAGGTTTCTGATGTCCGAGGGTTTGGTGCACAAGGTGGATCCAAAGAGAG 367
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                                                                                                                             29 AATCAIGGCGCGTCAATGACGAAACCCAICICAAIAACIICTCTCGGTTTCTAIICTGA
                                                   Gaps
                                                   33;
  Length 732;
                                                Indels
  DB 14;
  Score 458.8; DB 14;
Pred. No. 1.4e-85;
0; Mismatches 112;
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Brassica napus
  Query Match
Best Local Similarity 80.89
Matches 609; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="root"
/lab host="DH10B"
/clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2: Sall"
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//organism="Arabidopsis thaliana"
//mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL14-63-K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                           CD822497
BN25.045G20F020108 BN25 Brassica napus CDNA clone BN25045G20, mRNA
                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 Aagaacaacairtricrircricagairigcairtricgairircriggairtricgairtrichean 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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Unpublished (2003)
Contact: Genoplante
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1 (bases 1 to 669)
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/clone="BN25045G20"
/tissue type="seed"
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1. (Dases 1 to 451).

Seki, M., Narusaka, M., Ishida, J., Kamiya, R., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis tull-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). CDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall: This clone is in a modified Bluescript vector. Please visit our web
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AU226889 RAFL14 Arabidopsis thaliana CDNA Clone RAFL14-63-K15 3',
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details.
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    Pred. No. 2.1e-46;
; Mismatches 134;
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//organism="Vitis aestivalis"
//cullivar="Norton"
//cullivar="Norton"
//db xref="taxon:360s"
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/dev side="Y-B-112F06"
/tissue type="Leaf"
/dev side="Y-B-112F06"
/lab_bost="Xil0-Gold E.coli"
/lab_bost="Xil0-Gold
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                                                             212 AACAGAGCTCAAGAATGGTTTTTTTTTTTTTTTGGTCTCTAGATTCTGCGAAAAAT 153
                                                                                                                                                                                                                                                                                                                                 689 AATGAATGGAGTCTGTGTTTGGTTTCATGTTGAATCGATCAAGATGTGTTTTTAACTGTA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGAATTAIGCAGAAACAICTGTCCTGGTTCTCAGACAICGAAACTCTGTTCCTAATAA 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 CATGAATTATCCAGAAACATCTGTCCTGGTTCTCAGACATCGAAACTCTGTTCCTAATAA 33
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V-B-112F06 VAN-Baker-1 Vitis aestivalis cDNA clone V-B-112F06 5',
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                    AG--CGTGGGGAGAAAGCAGAGATGACTGGTGATATGCTTTCACCGTC
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Department of Fruit Science
Southwest Missouri State University-Mountain Grove
Southwest Missouri State University-Mountain Grove
Tel: 417 926 4105
Fax: 417 926 6646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 782)
Hou,H.S., Phanikanth,T.V., Kovacs,L. and Qiu,W.P.
Expressed sequence tags of young leaf tissues of
disease-resistant Vitis aestivalis var. Norton
Unpublished (2003)
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Insert Length: 782 Std Error: 0.00
Plate: VAN-Baker-1-12 row: F column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T3 PRIMER
High quality sequence stop: 782
POLYA=No.
                                                                                                                                                                         629 AACAGAGCTCAAGAATGGTTTTTTTTT
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Vitis aestivalis
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BQ798001 723 bp mRNA linear EST 30-JUL-2002 EST 6939 Ripening Grape berries Lambda Zap II Library Vitis vinifera cDNA clone RT093C02 3', mRNA sequence.
                                                                                                                                                                                                                   Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.

1 (bases 1 to 723)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Unite de Recherche des Produits de la Vigne
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 723
/organism="Vitis vinifera"
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/cultivar="Shiraz"
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33.1%; Score 270.6; DB 14; Length 782;

Query Match

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/mol_type="mRNA"
/cultivar="A17"
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                                                                 30.9%;
                                                                                                    Matches 308; Conservative
                                                                                     Similarity
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CA922829.1
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                                                       Query Mac.
                                                                    Match
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CA922829/c
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                             /dev_grage="ripering stage"
/dev_grage="ripering stage"
/clone lib="Ripering Grape berries Lambda Zap II Library"
/clone lib="Ripering Grape berries Lambda Zap II; Site_1: Eco
RI, Site_2: Xhol; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 bp mRNA linear BST 12-JUN-2003
AJ558383 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
AJ558383 Antirrhinum sequence.
AJ558383.1 GI:31660955
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                                                                                                                                                                                                                                                                                     186 AATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAATATCTTCTGATTATATTCCAGAC 245
                                                                                                                                                                                                                                                                                                                       919
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                                                                                                                                                                                                                                                                                                                                                                                             556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARGGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AAAGTTAAGATGGAAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACAAATA 485
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Lamiales, Antirrhinaceae, Antirrhineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 AAAGTCAAAATGGAGATTGTGGGGGAGCAAAGACCAGGTTGAAGCAGTAATTGACAAGATC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCA 545
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Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
Antirrhinum EST collection
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGTCATAAGAGTTAGGACAGGTGAGCGTGGGGAGAAAGCAGAAGATGACTGGTG 603
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                                                                                                                                                                                                              Score 262.8; DB 13; Length 723; Pred. No. 9.3e-45; 0; Mismatches 97; Indels 0;
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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/db_xref="taxon:29760"
/clone="RT093C02"
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/db_xref="taxon:4151"
/clone="018_1_07_f22"
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Antirrhinum majus
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                                                                                                                                                                                                            32.2%;
76.8%;
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Best Local &
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                            264 GAAGCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                       291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 ATTCGAGGTGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 GGAGAGATTGGTGATGGGAAGATTTTTGTGCTTCCAGTTTCTGATGTAATAGAGTTCGC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 812)
VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Aken, S.,
Utterback, T., Cheung, F. and Praser, C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and
re-arrayed from various libraries
                                                                                                                                                                                                                                                 204 CCTGTCGTTAGTGCCCAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 GTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACA
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EST640547 MTUS Medicago truncatula cDNA clone MTUS-58H7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                   ő
                                                                                                                        732;
/tissue_type="whole_plant"
/clone_lib="Antirrhinum_majus_whole_plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.medicago.org
                                                                                                                        Length
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 ACAGGTGAGCGTGGGGAAAAGCAGAGAAGATGACTGGTG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 ACTGGTGAACGAGGGAAAAGGCTGAGAGGATGGTGGGGAG 571
                                                                                                                                                                                   92;
                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kvandenb@cbs.umn.edu
Alias Clone pMHRP-28F3
TIGR sequence name: MTUCF91TV
More information is available at: www.med
Seq primer: (gtA AtA CgA CtC ACt AtA ggg
Location/Qualifiers
                                                                                                                     Score 252.8; DB 9
Pred. No. 1.1e-42;
0; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 bp
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USA

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liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. CDNA was prepared from polyAppooled for mRNA extraction. CDNA was prepared from polyApten Unizap XR vector from Stratagene and packaged using digapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone lib="GBSD"
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript Site 2: EcoRI; Site 2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regegarreaggierracigilictealgregaggerriegigeacakaggaggiiera 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AAATAGTGGTGAGAAAAGACCAGGTTGAGGCAGTGATAAACAAAATTATGGAGACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACAGGAGAGTTGGTGATGGCAAGATTTTTGCTTTTGCCTGTGTCAGATGTCATAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGAGAGACACGGTGGCTCTGGGAAGACAAATTTGTTGCTAAAGTTAAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3880"
/clone="pdBSD914"
/fissue_type="immature seeds"
/dev stage="immature seeds, 11 to 19 days after
pollInation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.3%; Score 247.8; DB 12; Length 714; Best Local Similarity 67.6%; Pred. No. 1.2e-41; Matches 348; Conservative 0; Mismatches 167; Indels 0;
                                                                                                                                                                                                                                  TIGR sequence name: MTPAP50TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                  TX 77030-2600,
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 TGCGAATAATAATGAATGGAGTCTGTGTTTGGTTT
                                  1100 Bates Street, Houston,
Tel: 713-798-7044
Medicine
                                                                                                                                                            Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="A17"
                                                                                                                 Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
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                                                                                                                                                                                                            /clome lib="MTUG"
/clome lib="WTUG"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK-; Site 1: EcoRI, The CDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 partagrogrogropapapagaccaggrroaggrogropapacapartrarggagggoggopa 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aacircaadccaircicaeccarecaeariccrcaecriricricecriricricaeaa 504
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ESTs from developing reproductive tissues of Medicago truncatula (Uppublished (2001))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAGGACAGGTGAGGGTGGGGAGAAAGCAGAAGAAGATGACTGGTGATATGCTTTCACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T14 bp mRNA linear EST EST5312822 GESD Medicago truncatula cDNA clone pGESD904 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 249.6; DB 14; Length 812;
Pred. No. 5e-42;
0; Mismatches 139; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
                                                                                                    tissue_type="mixed tissues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 CTTAGGAACAAACAGAGCTCAAGAATGGTTTTTT
                                                                                                                              /dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula (barrel medic)
                     /db_xref="taxon:3880"
/clone="MTUS-58H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI311072.1 GI:14985399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 333; Conservative
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BI311072
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TAMU Lycopersicon esculentum cDNA clone
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//clone lib="tomato callus, TAMU"
//note="Yector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 ITCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCATGGAG 286
                                                                                                                                  353 AAGAGAGGAGGAGGCTCCGAATTTTCTGAAGACAATTTTGTTGCCAAAGTTAAAATGG 412
                                                                                                                                                                                                                                           473 gaacrossgagarrogrograficaritricricarccristarcroardrafia 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamids, Solanales, Solanaceae, Solanum, Lycopersicon.
293 TGGGAATTCGTGTGTCACTGTATCTGATGTCAAGGGGTTTGGTGCTCAGGGTGGCTCAA 352
                                                                  379 CCGAGAGACACGGGTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGG 438
                                                                                                                                                                                                     AAAICGITGITAAGAAAGACCAAGIGGAAICTGIAAICAACACAAIAAITGAAGGAGCAA 498
                                                                                                                                                                                                                                                                                                                                          GGACAGGAGATTGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAG 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 gerchecerreaadegerereaaangereererrerreeegarrareaagegeegaare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ronning, C.M., Frager, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         559 TTAGGACAGGTGAGCGTGGGGAGAAAGCAGAAGATGACTGGTG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 ICCGCACAGGTGAGCGTGGGGAGCTGAGAGGAGGATGGCTGGGG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cch 30.0%; Score 245; DB 9; Length 61:
al Similarity 72.5%; Pred. No. 5.1e-41;
317; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Lycopersicon esculentum"
/mol type="mRNA"
/coltvar="TA496"
/db xref="taxon:4081"
/clone="cLEC36D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giovannoni,J.
Generation of BSTs from tomato callus tissue
Unpublished (1999)
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/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum (tomato)
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//clone lib="Wetcor: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//clone lib="MMAD"
//clone lib
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                                                                                                                                                                            BE239550 S97 bp mRNA linear EST 12-JUL-2000
EST403599 MHRP- Medicago truncatula cDNA clone pMHRP-28F3, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AGGIGGAAGCAAITGICAGACCATGGAGAAICCAGCAAGTTICAICGGCTITACIGAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 ITITACCIGICGITAGICCCCAAATAICTICIGAITATATICCAGACTCGAAAITITACA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 TICTICCCAAAATCAGAGCTCAAAACCTICCTGACTATGTTCCTGAATCCAAGTTTTACA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AAGTIGAAGCCATICTCAGGCCATGGAGAATCCCTCAGGTTTCTTCGGGTTTGTTGAAAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, T.E., Cho, J. and Fraser, C.M.

ESTS from phospate starved roots of Medicago truncatula Unpublished (2000)
Contact: Maria J. Harrison
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Parkway, Ardmore, OK 73401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 580-221-7380
Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N265417e
TIGR sequence name:MTHAC26TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   More information is available at. . http://chrysie.tazu.edu/medicago seq primer: SKmod [CTA gAA CTA gtg gAT CC] Location/Qualifiers
              652 GAATTGATAACAATGATGTATGTTGTGTGTATTTT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Medicago truncatula"
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/dev_stage="phosphate-starved"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula (barrel medic)
Medicago truncatula
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cultivar="A17"

db xref="taxon:3880"
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Best Local Similarity 75.6°
Matches 306; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

[ Dases 1 to 702)
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                                                                                                        251 AATTCAACAGGTTTCTTCGGCACTACTGAAATGGGCATTCGTGGTGTCACTGTTTCGGA 310
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/dev stage="buds 8mm to preanthesis"
/dev stage="buds 8mm to preanthesis buds"
/clone lib="tomato flower. 8 mm to preanthesis buds"
/clone lib="tomato flower. 8 mm to preanthesis buds"
/note="Weetor: pBluescript SK!-); Site_1: BcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                                                                                                                                                                                 347 IGIGAGAGGGTITGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTC
                                                                                                                                                                                                                                          467 ATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                      527 ITITIGITITIGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGGAGAAAGC
                                                                  287 AATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGGATTCGAGGTGTTACTGTTTCTGA
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/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
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Score 245; DB 12; Length 7 Pred. No. 4.8e-41; 0; Mismatches 120; Indels
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Search completed: May 28, 2004, 00:14:51 Job time : 1898.7 secs

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May 27, 2004, 13:35:34; Search time 2651.35 Seconds [without alignments] 14663.718 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1		÷ {			SUMMARIES	
No.	Score	Match	Length	DB	ŒΙ	Description
	897	0	897	ı	AR125590	AR125590 Sequence
7	840	9	840		AF095454	AF095454 Ricinus c
m •	594	CI L	594		AR125592	AR125592 Sequence
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7	285	ω (	588		AR125591	AR125591 Sequence
00 C	285	20 O	591		AX507438 properties	AASU/438 Sequence BEOGESIG Brabidons
, <u>-</u>	277.4	30.9	947		AY442185	AY442185 Lycopersi
11	217.2	24.2	902		AK068407	AK068407 Oryza sat
12	217.2	24.2	902		AK099152	AK099152 Oryza sat
13	215.4	24.0	1085		PPI489604	AJ489604 Pinus pin
14 17	703	11.9	686 2492		AF01/417 ASD051R00	Aroilti Noscoc pu Arosi822 Anabaena
C 16	103.2	11.5	341880		AP003589	AP003589 Nostoc sp
-	66	11.0	384		FDGLNBPRT	X97327 F. dipiosiph
	98.8	11.0	191028		PPU38804	U38804 Porphyra pu
0 19	96.4	10.7	110000		067574 AR271569 03	Continuation [2 of
21	96.2	10.7	10338			U67464 Methanococc
c 22	96.2	10.7	110000		AR271569_14	Continuation (15 o
23	95.4	10.6	383		SYOGENE	M62447 Synechococc
24	95.4	10.6	4348		AP079137	Ar079137 Synechoco
255	4.4	n n	130001		556LNBP 1190915	D90915 Synechocyst
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c 28	90.4	10.1	164921	60	AF022186	AF022186 Cyanidium
U 70	-	H (	299350		AP005370	AFOUSSIU IDETHOSYLL DEGALODE Wibrich
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					ALIGNMENTS	
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DEFINITION			14 from	patent	US 6177275.	
ACCESSION VERSION			1 GI:14	1111	652	
KEYWORDS						
SOURCE		Unknown. Unknown.				
REFERENC		Unclassified 1 (bases 1	ied. 1 to 89	17		
AUTHORS TITLE		uzzi, nt ni	G.M., Lam,H. itrogen regul	n, H.	-M. and Hsieh, MH. latory P-PII genes	
JOURNAL FEATURES		cent: US	S 6177275 Location/	75-A 1/0u	5-A 14 23-JAN-2001; /Oualifiers	
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dykgpgagacyterqagsbesedkfykykkelvvskooybedvieklibeartgeigd
gkiplidvsdvikkytobrodkaernyggrsdmstsa"
                                                                                         Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Malpighiales, Euphorbiaceae, Acalyphoideae;
Acalypheae, Ricinus.
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.
A PII-like protein in Arabidopsis: putative role in nitrogen
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M.
Direct Submission
Submitted (29-SRP-1998) Biology, New York University,
Washington Square Bast, New York, NY 10003, USA
Location/Qualifiers
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/function="putative role in nitrogen sensing"
/note="GLB1"</pre>
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99030678
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100.0%; Pred. No. 4e-197;
ive 0; Mismatches 0; Indels
   cds.
   Ricinus communis PII protein mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                    organism="Ricinus communis"
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                                                              Ricinus communis (castor bean)
Ricinus communis
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Pred. No. 3.1e-211;
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/organism="unknown"
/wol_type="unassigned DNA"
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PLN 19-NOV-1998

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(Gases 1 to 796)

Garcia-Ibilcieta,D. and Sengupta-Gopalan,C.

Direct Submission

Direct Submission

New Mexico State
Submitted (12-FBB-2001) Molecular Biology Program, New Mexico State
University, Corner of Knox and College, Las Cruces, NM 88003, USA

Location/Qualifiers
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IFLIPVSDVIRIRTGERGEQAERMAGGLTDALYV"
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                                                                                                                                            421 GACCAGGTTGAGGATGTTATAGAAAAATCATTGAGGAGGCAAGAACAGGAGGAGATGGA 480
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Medicago sativa
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceee; Papilionoideae; Trifolieae;
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361 TCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAA
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                                                 410 TCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAA
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Medicago sativa PII protein (GLNB) mRNA, complete cds.
AY027892
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Pred. No. 1.8e-63;
0; Mismatches 153; Indels
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Characterization of PII (GLNB) in alfalfa
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/gene="GLNB"
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CGGCAAGATTTTCTTGCTGCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGG
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Best Local Similarity 100.0%; Pred. No. 3.2e-136;
Matches 594; Conservative 0; Mismatches 0; Indels
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
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Pacent: US 6177275-A 16 23-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 from patent US 6177275.
AR125592
AR125592.1 GI:14111654
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/organism="unknown"
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VSDVRGFGAQGGSTERHGGSBFSEDKFVAKVKMB1VVKKDQVESVINT1IEGARTGEI
GDGKIFVLPVSDVIRVRTGBRGEKAEKMTGDMLSPS**
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                 268 caariigicakooriosakaaricakooaksiiroariosooriiracisaaaaarossariic 327
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                                                                                                328 GAGGTGTTACTGTTTCTGATGTGAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACAC
CAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAAATTGGTATTC
                                                                                                                                             AGGGCGCCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGG
                                                                     GAGGTGTTACTGTTTCTGATGTTCGAGGTTTTTGGTGCTCAAGGTGGTTCAACTGAGAGGC
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Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.
A PII-like protein in Arabidopsis: putative role in nitrogen
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Hsieh, M.H., Lam.H.M., van de Loo,F.J. and Coruzzi,G.M.
Hsiert Submission
Submitted (29-5EP-1998) Biology, New York University, 100
Washington Square East, New York, NY 10003, USA
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/product="PII protein"
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                                     24 GIGGICCIAAGAAGCAACGGAAAIGCIICGGIICIIICCCAAAAIIAGAGCICAAAACCII
                                                                           242 CCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGA
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Coruzzi, G.M., Lam, H.-M. and Hsieh, M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 13 23-JAN-2001;
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/mol_type="unassigned DNA"
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                            CAAAGCICGCCIGACIACAITCCIGAIGCIAAAIICIACAAAGIGGAAGCAAITCICAGG
                                                                                                247 ccarodadarccadcaadrircarcodcirracroadaarcodoarrcoadgiracr
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TITAACACCGCGGTCAAGCGCGTAAGATATGCC----CCCGTCGTTCCTGTGATTAATGCC
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 2133 28-FBB-2002;
The Scripps Research Institute (US); Syngenta Participations (CH)
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    /organism="Arabidopsis tha
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    GAATTCGGCACGAGGCTACTGCGAAACTGGGCTTGCTCACTCCTCTTCATTCTAATAACA 104
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                          GAATCATGGCGCGTCAATGACGAACCCATCTCAATAACTTCTTCTGTTTCTATTCTG
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/procein_id="AA063273.1"
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LVTKSPSRNSRVLPVYSAQISSDYIPDSKFYKVRALVRPWRLQQVSSALLKIGIRGVT
VSDVRGFGAQGSSTRRHGGSEFSEDKFVAKVKABIVVKKDQVBSVINTIIEGARTGEI
                                                                                                                                                                                                                                         Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
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          The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim.C.J., Chen.H., Cheuk.R., Shinn,P., Bowser,L., Chan, M.M., Chang, C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Liam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="At4g01900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="U23463"
/ecotype="Columbia"
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1 (bases I to 591)

1 (bases I to 591)

2 (chan, H., Chenk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Couach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to (bases 1 to 591)
Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Carninci,P.,
Chan,M.M., Chang,C.H., Dale,J.M., Hayashizaki,Y., Hsuan,V.W.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Ishida,J., Lee,J.M., Iin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Sarcu,M., Seki,M.,
Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K.,
Ecker,J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                             367 GAGTICTCGGAAGACAAATITGTTGCTAAAGITAAGATGGAAATCGTTGTTAAGAAAGAC 426
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CTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTTACCTGTCGTTAGTGCC
                                                   CAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGG
                                                                                     187 CAAATAICTICTGGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTGAGA
                                                                                                                                                   CCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAAATTGGTATTCGAGGTGTTACT
                                                                                                                                                                                                                                                    GAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana At4g01900 mRNA, complete cds.
Br005209
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Arabidopsis thaliana
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Unpublished
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ACCESSION
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246 352

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4.86 592 545

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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ouneda, E., Yahagi, W., Suzuki, K., Lii, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Muzkami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Y., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Narimekawa, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mizura, J., Kawai, J., Carninci, P., Adachi, J., Alzawa, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Riken:, Kawai, J., Kando, S., Konno, H., Miyazaki, A., Osato, N., Inctani, K., Ishii, Y., Itch, M., Saito, R., Saito, R., Shibata, K., Shinagawa, A., Shiraki, T., Volino, M. and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shiraki, T., Volino, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                 JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J013149B08, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collection, mapping, and annotation of over 28,000 cDNA clones from
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FIL CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Virdigləİnince; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; İiliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
                                                                                          CTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGGGTGATAAGGCTGA 603
                                                                                                                                                                                                                604 GAGGATGACAGGAGGCGATCTGACATGAGTACTTCTGCTTGACTGCTGTGACCAGCAA 662
                                                                                                                                                                                                                                                                        601 GAGGATGATGGGGGGCATGCTGATATGTCCTCTGCATTATCAACTTCTTGAGCGGCAA 659
japonica rice
Science 301 (5631), 376-379 (2003)
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VRGFGAQGGIJERQAGSEFSEDTFVAKVYMEIVVSKDQVEGVIAKIIERARTGEIGDG
KIFLTPISDVIRVRTGERGEKAERMMGGHADMSSALSTS"
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                                                                                                                                                                                                                                            AY42185 947 bp mRNA linear PLN 15-NOV-2003 Lycopersicon esculentum PII-like protein (GLB1) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; viridiplantae; Streptophyta; Euchoryledons; core endicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases I to 947)
Ralch-Liu, P., Roemheld, V. and von Wiren, N.
A PII-like protein in tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cases 1 to 947)
Walch-Liu,P., Roemheld,V. and von Wiren,N.
Direct Submission
Submitted (17-CCT-2003) Institute of Plant Nutrition, Hohenheim University, Fruwirthstr. 20, Stuttgart 70593, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 CGCGGTCAAGCGCGCTAAGATATGCCCCCGTCGTTCCTGTGATTAATGCCCAAAGCTCGCC
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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PII-like protein"
/protein_id="AAR14689.1"
/db_xref="GI:38231570"
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                                                                                                547 GAGAAAGCAGAGAAGATGACTGGTG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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                                                                                                                                                                        NIAS Rice Full-Length CDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
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   Laboratory of Gene Expression; 2-:-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:8fikuchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 cakceneceseenniceseekakaaseeseentakenakaaseenakaaseentakakin 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
mol type="mRNA"
/cultivar="Mipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 6.3e-43;
0; Mismatches 128; Indels
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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satok, K., Magata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satok, Y., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahadi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Inda, R., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sudiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mirua, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshino, M. and Hayashizaki, Y., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Shinagawa, A., Shiraki, T., Collection, mapping, and annotation of over 28,000 cDNA clones from apponica rice
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Oryza sativa (japonica cultivar-group) cDNA clone:J023070H02, full insert sequence.
                                                                                                                                                                                                                                                                     FII_CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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This clone is one of the 28K full-length cDNA clones from japonica
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NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
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E-29071,

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SKVKMIIVVSKOQVBAVIDALIDSARTGBIGDGKIFVVPVADVIRVRTGERDLKPERM
AJ489604.1 GI:37653226
glb gene; PII-like protein.
Pinus pinaster
Pinus pinaster
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinus; Pinus; Pinus.
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Submitted (11-JUN-2002) Canton F.J., Molecular Biology and
Biochemistry, Faculty of Sciences, Campus de Teatinos s/n,
                                                                                                                                                                                                                 A PII-like protein from xylem of adult Maritime pine trees
Unpublished
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Pred. No. 1.8e-42;
0; Mismatches 101; Indels
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/product=*PII-like_protein"
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/db_xref="GI:37653227"
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/dev stage="adult tree"
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/db_xref="taxon:71647"
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    Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 ANIATITITICATACCCGIGICGACGIGAICAGAATACGCACCGGCGAACGAGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism=*Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/docteivar=*Nipponbare"
/db xf=txaon:39947"
/clone="J023070H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 217.2; DB 8; larity 69.7%; Pred. No. 6.3e-43; Conservative 0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629
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Gaps

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Length 1085;

206

601

687 GAGAGAATGGCTGGTGG 703

linear PLN 11-OCT-2003

PPI489604 linear loss bp mRNA linear linear lines pinus pinaster mRNA for PII-like protein (glb gene).

LOCUS DEFINITION

RESULT 13 PPI489604

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BCT 15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GOA: 09L422"
/db_xref="SPTREMBL: 09L422"
/translation="MKKVEAIIRPFKLDEVKIALVNAGIVGWTVSEVRGFGROKGQTE
RYRGSEYTVEFLQXLKVVEIVVEDNQVDMVVDKIIAAARTGEIGDGXIFISPVEQVIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1073 AATGAAAAAAGTAGCTATTATCGCCCATTAAGCTAGATGAAGTGAAATCGCTTT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1250 GAAGGIGGAGATIGITGITGAAGATAACCAAGTIGATATGGTTGTTGACAAAATCATTGC 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 GCTAAAATTGGTATTCGAGGTGTTACTGTTTCTGATGTTCGAGGTTTTGGTGCTCTAAGG 384
                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (14-DEC-1999) Zhang C.C., Laboratoire de Chimie
Bacterienne, C.N.R.S., 31, chemin Joseph Aiguier, 13402 Marseille
cedex 20, FRANCE
                                                                                                                                                                                                            Gonzalez,L., Phalip,V. and Zhang,C.C.
Phosphorylation of the signal transduction protein PII by the
Ser/Thr kinase PknC in the cyanobacterium Anabaena sp. strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1310 recrectorracadeceaaarcesrearegraaaarcritarcreaccieragaacaagr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 ATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 IGGITCAACTGAGAGGCAGGGCGGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1193 AGGACAGACAGAACGCTATCGCGGCTCTGAGTACACTGTGG----AGTTTCTGCAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 TAAGATGGAGATCGTGGTTAGCAAAGACCAGGTTGAGGATGTTATAGAAAAAATCATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 GGAGGCAAGAACTGGAGATTGGAGACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGT
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                                    linear
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                                  ASP251822 2493 bp DNA line
Anabaena sp. PCC7120 glnB gene for PII protein.
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                                                                                                               glnB gene; PII protein.
Nostoc sp. PCC 7120 (Anabaena sp. PCC 7120)
Nostoc sp. PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103.2; DB 1;
Pred. No. 1.1e-14;
0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCC 7120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="signaling protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="PII protein"
'protein id="CAB75358.1"
'db xref="GI:6983587"
                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .2493
/organism="Nostoc sp. PC
/mol_type="genomic DNA"
/strain="PCC 7120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db xref="taxon:103690"
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Llarity 58.5%;
Conservative 0
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/gene="glnB"
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2 (bases 1 to 2493)
2hang, C.C.
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AUTHORS
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RYRGSEYTVBFLQKLKVEIVVDDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRI
RTGEKNTEAV"
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                                      BCT 15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 AAAGGCCAAACTGAACGGTATCGCGGTTCTGAGTACACCGTTG---AGTTTTTGCAAAAA 448
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                                                                                                                                                                                                              Hanson,T.E., Forchhammer,K., Tandeau de Marsac,N. and Meeks,J.C. Characterization of the glinB gene product of Mostoc punctiforme strain ATCC 29133: glnB or the PII protein may be essential Microbiology 144 (Pt. 6), 1537-1547 [1998]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATGAAAAAAGTAGAAGCTATTATCCGCCCATTTAAGCTAGATGAGGTAAAAATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 TIGCIAAAATIIGGIAIICGAGGIGIIACIGIIICIGAIGIICGAGGIIIIIGGIGCICAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 GGTGGTTCAACTGAGAGGCAGGCGGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 CTCAAAGTGGAAATCGTCGTTGACGACAATCAGGTTGATATGGTGGTGGAAAATTATT
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                                                                                                                                                                                                                                                                                                                                                Harson, T.E. and Meeks, J.C.
Direct Submission
Submitted (05-AUG-1997) Section of Microbiology, University
California, One Shields Avenue, Davis, CA 95616, USA
                                                                                                                                                                          Bacteria; Cyanobacteria, Mostocales; Nostocaceae, Nostoc.
1 (bases 1 to 686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="glnB"
'function="putative nitrogen regulatory protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 107; DB 1; Length 686; 60.4%; Pred. No. 1.2e-15;
                          Arv1/419 686 bp DNA linear Nostoc punctiforme PII (glnB) gene, complete cds. AF017419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/strain="ATCC29133; PCC 73102"
/db_xref="ATCC:29133"

    . 686
    /organism="Nostoc punctiforme"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="AAC26348.1"
db_xref="GI:2394288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:63737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAATAAGAGTCCGCACTGGTGA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGATICGGALICGIACIGGCGA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/transl_table=11
/product="PII"
                                                                                                 GI:2394287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="glnB"
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                                                                                                                                       Nostoc punctiforme
                                                                                                                                                            punctiforme
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Best Local
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  RESULT 14
AF017419
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TITLE
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## ALIGNMENTS

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters. Castor bean, PII; plant nitrogen regulatory gene, P-PII; nitrogen assimilation; transgenic plant; herbicide screening; ss. BP Hsieh M; 97US-00899330. 96US-0022328P. AAF58582 standard; cDNA; 897 Ricinus communis P-PII cDNA. (UKNY ) UNIV NEW YORK STATE. Coruzzi GM, Lam H, WPI; 2001-158572/16 Ricinus communis. P-PSDB; AAB69496 US6177275-B1 23-JUL-1997; 24-JUL-1996; 23-APR-2001 23-JAN-2001 AAF58582; RESULT 1 AAF58583 

The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

Claim 2; Fig 13; 35pp; English.

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Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                        Castor bean; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening;
                     Ricinus communis P-PII cDNA fragment
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                                                                                                                                                                                                                                                                           Sequence 594 BP; 149 A; 117 C; 157 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           A; 117 c; ...
66.2%; Score 594; DB 4; Lengta ...
7. 4. Pred. No. 5e-137; 0; Indels
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nes 594; Conservative
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AAF58584

RESULT 2
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ID AAF5:
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AC AAF5:
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AAF58584

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GGTTTTCTCACTTTAACACCGCGGTCAAGCGCGTAAGATATGCC---CCCGTCGTTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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ID AAF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 GAATTCGGCACGAGGCTACTGCGAAACTGGGCTTGCTCACTCCTCTTCATTAACA 104
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                                                  GACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGG
                                                               GACCAGGITGAGGATGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGATTGGA
                  GACCAGGITGAGGATGITATAGAAAAAAAAAAAGGAGGAGGGAAGAAGAACTGGAGGATGGA
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                                                                                                   643
                                                                                                                          541 SETCATAR SECTEAGRAGGATER CAGGAGGCGATCTER CATERCITCTGCT 594
                                                                                                                                                                                                                                                                                         gene; P-PII;
                                                                                                                                                                                                                                                                                         Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening; ss.
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                                                                                                   GGTGATAAGGCTGAGAGGATGACAGGAGGGCGATCTGACATGAGTACTTCTGCT
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                                                                                                                                                                                                                                                                   Arabidopsis thaliana P-PII cDNA.
                                                                                                                                                                                          AAF58581 standard; cDNA; 817 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lam H, Hsieh M;
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P-PSDB; AAB69495.
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Best Local Similarity
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148 GACCATÓTIGOCTOGAITIGGICACAAÁGICACGGÁGIAATAACAGIÓGIGITITAACÍG
                                                                                                                                                                                                                                                                                                                                                                                                                                               388 ACGGTGGCTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATCGTTG
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                                                                                 TGATTAATGCCCAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAG
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transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                                                                                Query Match
31.8%; Score 285; DB 4; Length 588;
Best Local Similarity 70.3%; Pred. No. 1.5e-60;
Matches 397; Conservative 0; Mismatches 165; Indels
                                                                           Sequence 588 BP; 164 A; 105 C; 147 G; 172 T; 0 U; 0 Other;
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24-AUG-2001; 2001WO-US026685

28-FEB-2002

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell production of transgenic plants. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to absolic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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70.3%; Pred. No. 1.5e-60;
tive 0; Mismatches 165; Indels
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                                                                                                                                                                                                                                                                                                                                                               Zhu T;
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                                                                                                                                                                                                          (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                               Wang X,
24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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Best Local Similarity 70.3
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Harper JF, Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-304127/34.
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                                                                                                                                                                                                                                                                                                                                                                                                 13167 TGTTATTGATATCATATGCGAGAATGCAAGAACAGGAAACCCCAGGAGATGGAAAAATCTT 13108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions, and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                              544 CTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGGTGATAAGGC 600
                                                                                                                                           244 TGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGT
                                                                                                                                                                      13404 TTATAAAAATGAGGTTGAGATTATGAAAAAAGTTGAAGCAATCATAAGACCGGAGAAGTT
                                                                                                                                                                                                                             13344 GGAGATTGÍTAAAAAGGCTÍTTGTCTGATGCTGGGTATGTTGGAATGACTGTTAGTGAGGT
                                                                                                                                                                                                                                                         424 AGACAAGTITGITGCTAAAGTIAAGAIGGAGAICGTGGTTAGCAAAGACCAGGTTGAGGA
                                                                                                                                                                                                  304 CTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTCTGATGT
                                                                                                                                                                                                                                                                                                                                                                        TGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGATTGGAGACGGCAAGATTTT
                                                                                                                Gaps
                                                                                    Length 110000;
                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic library for identifying diagnostic and therapeutic and for identifying virulence factors, regulatory elements targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                               0; Mismatches 153; Indels
                                                                                   Score 96.2; DB 2;
Pred. No. 4.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bronchopulmonary; endocarditis; meningitis; ss
             1410000
1510000
1610000
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  1310000
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1300001
1400001
1500001
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                                                                                                                  201; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic fragment #35
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                                                                                                    Similarity
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AAV21209_12
AAV21209_13
AAV21209_14
AAV21209_15
AAV21209_16
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                                                                                       Query Match
                                                                                                   Local
                                                                                                                  Matches
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LOCUS AAV21209 Accession Aav21209
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Pred. No. 4.4e-13;
0; Mismatches 136;
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   specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
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is useful for aidentifying diagnostic and therapeutic
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                                                                                                                                                                                                                                                          Seguence 96109 BP; 28783 A; 18910 C; 20341 G; 28075 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                            Score 84.8; DB 4; Length 96109;
Pred. No. 3.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGAATTTGATGAAAGTGC 13269
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Best Local Similarity
Matches 180; Conserv
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                                 The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 raccecececreararererrar---rrcraecraaeraaareaarrece
                                                                                                                                                                                                                                                                                                                                GCAATTGTAAAACCGTTTAAATTGGATGATGGCGTGAAGCACTCTCTGACATTGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGATTGGAGACGCCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 AAAATCGGCGACGGTAAGATTTTTGTGACTAATCTGGAACAAGTCATCCGTATCCGTACA
                                                                                                                                                                                                                                                                                                  GCAATICTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAAATTGGTATT
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                                                                                                                                                                                                                                  Length 375;
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                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                     Sequence 375 BP; 122 A; 64 C; 93 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens nucleotide sequence #10494
                                                                                                                                                                                                                                  Score 83.6; DB 8;
Pred. No. 9.2e-11;
0; Mismatches 139;
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LOCUS ACF67367 Accession Acf67367
                                                                                                                                                     proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypetrides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. cecombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The cecombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens and the proteins are as virulence biopesticides. Other uses of the genes and the proteins are as virulence are sensitive to P. luminescens and indicates for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
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                                                               sequence of Photorhabdus luminescens and encoded polypeptides,
                                                                               e.g. as therapeutic antimicrobials and agricultural pesticides,
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                                                                                                                                           genes and their encoded
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Pred. No. 3.1e-10;
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                                                                                                                                             The invention relates to the isolation of
                                                                                                             Claim 2; SEQ ID NO 10494; 1205pp; French.
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Continuation (53 of
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                                                                                                                               270 ACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAA
                                                                                                                                                                    63919 AAAAATCGAAGCAATGATTAAACCCTTTAAATTAGACGATGTGCGAGAAAGTCTTTCAG
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                                           Length 110000;
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                                                                                    0; Mismatches 139;
                                         Score 77.6; DB 2;
Pred. No. 2e-08;
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1830121
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                                      Query Match
Best Local Similarity 55.1%;
Matches 174; Conservative
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Pred. No. 2.3e-09;
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                         Score 77; DB 7; Length 363;
Pred. No. 3.9e-09;
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al Similarity 54.1%; Score 77; DB 7; Length 363
al Similarity 54.1%; Pred. No. 3.9e-09;
180; Conservative 0; Mismatches 150; Indels
Sequence 363 BP; 84 A; 77 C; 123 G; 79 T; 0 U; 0 Other;
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent

Isolated nucleotide sequences of Neisseria meningitidis which can be in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorthoea.

Tettelin H, Venter JC; Ratti G, Scarselli M, Scarlato V;

ickey E, Peterson J, Galeotti C, Mora M,

Hickey E,

(CHIR ) CHIRON CORP.

'V, Gar. P. Pizza M;

Masignani V, Rappuoli R,

WPI; 2000-318079/27.

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cc specifically claimed Neisseria meningitidis genomic DNA sequences;
AAA81260 to AAA81303 and AAB25620 to AAB2563 represent Neisseria DNA
sequences and their corresponding proteins; AAA8124 to AAA81259 and
AAA81304 to AAA8121 represent PCR primers used in the isolation of
Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent
CC Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent
CC Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent
CC Neisseria meningitidis DNA sequences; and an uncleic acid
cused in the exemplification of the present invention. The nucleic acid
csequences, protein sequences, and antibodies against them, can be used in
the manufacture of a composition can be used as a
medicament (or in the manufacture of a medicament) for treating,
preventing or diagnosing infection due to Neisserial bacteria. For
example, some of the identified proteins could be components of vaccines
cc example, some of the identification of sequences from the bacterium
will also facilitate production of biological probes, particularly
cc organism-specific probes, Attempts to make efficacions Meningococcus B
cvaccines have failed mainly due to antigen tolerance. Multivalent
cvaccines have also been tried but none have successfully overcome
cc antigenic variability. The provision of futher, complete sequences may
crowide an opportunity to identify secreted or surface exposed proteins
cc that may be presumed targets for the immune system and which are not
considered.
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Pred. No. 1.4e-07;
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BM13473 EST561009 BM33234 EST561009 BM32334 AJ553383 AW035791 EST264195 BM32123 EST254179 BM33123 EST552012 AW738071 EST399498 BM33034 EST550225 BM33034 EST550225 BM33034 EST550225 BM33034 EST560225 BM3036 EST549949

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cr8652 lambdaZAPST Ricinus communis cDNA clone pcr8652 similar to nitrogen-regulatory protein, mRNA sequence.
T15252 T15252.1 GI:14190796
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1 (bases I to 542)
vandeLoo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St., Stanford, CA 94305
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Ricinus communis
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TITLE
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Copyright (c) 1993 - 2004 Compugen Ltd.
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'clone="V-B-112F06"
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 Department of Fruit Science
                                  Tel: 417 926 4105
Fax: 417 926 6646
Email: weq070f@smsu.edu
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                                                                                                                                                                                                    Score 408.8; DB 14; Length 542;
Pred. No. 1.7e-54;
0; Mismatches 18; Indels 2:
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Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P. Expressed sequence tags of yourg leaf tissues of disease-resistant Vitis aestivalis var. Norton Unpublished (2003)
Contact: Wenping Qiu
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Best Local Similarity
Matches 428; Consert
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/issue type="feat"
/dev stage="feat"
/lab_host="Young leaf"
/lab_host="XL10-Gold E .coli"
/clone lib="VAN-Baker-1"
/clone lib="VAN-Baker-1"
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grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves (Vitis. aestivalis var. Norton). The cDNA synthesis and library construction was performed according to the instruction manual for pBluescript II XR cDNA library construction kit provided by Stratagene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 ACGGCAAGAITITICTIGCTGCCTGTITCAGAIGIAATAAGAGTCCGCACTGGTGAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAATTGCCTCTCATAGACTGCACTTTGATCCGCCCCAATCTCAAAGATTCTCGAAATT
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Southwest Missouri State University-Mountain Grove 9740 Red Spring Road, Mountain Grove, MO 65711-2999, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atch 35.8%; Score 321.4; DB 14; Length cal Similarity 73.7%; Pred. No. 5.7e-41; 409; Conservative 0; Mismatches 146; Indels
                                                                                                                                                    90
                                                                                                    Plate: VAN-Baker-1-12 row: F column: Seg primer: T3 PRIMER High quality sequence stop: 782 POLYA=No.
                                                                                                                                                                                                                                                                                           /organism="Vitis aestivalis"
/mol_type="mRNA"
/cultivar="Norton"
                                                                                                                                                                                                                                                                                                                                                                               'db xref="taxon:3605"
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244

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/clone lib="MHRP-"
//clone lib="MHRP-"
//clone lib="Wector: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//clone lib land land state for an analysis of a further state of an analysis of a further state of an analysis of a further state weekly with 1/2 Hoadlands solutions containing 20um potassium phosphate. CDNA was prepared from polyatenticked RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using interest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                        363 AGGACTGGAGGATTGGTGATGGCAAGATCTTTTGGTGCCCATATCGGATGTGATAAGA 304
                                                                                                                                                                                                                                            572 GICCGCACTGGIGAGCGGGGTGATAAGGCTGAGGGATGACAGGAGGGCGATCTGACATG 631
BE219550 597 bp mRNA linear EST 12-JUL-:
EST403599 MHRP- Medicago truncatula cDNA clone pMHRP-28F3, mRNA
                                                                                                                                                                                                                                                                                       512 AGAACTGGAGAGTTGGAGACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hansi
Holt, I.E., Cho, J. and Fraser, C.M.
ESTs from phosphate-starved roots of Medicago truncatula
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N265417e
TIGR sequence name:WTHAC26TK
Acre information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
1. 597
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/dev_stage="phosphate-starved"
/lab_host="XLOIR"
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Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Maria J. Harrison
Plant Biology Division
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EST 6939 Ripening Grape berries Lambda Zap II Library Vitis
vinifera cDNA clone RT093C02 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 crcanagarrereganarrecagriraarregeeeranaeedeerenaagaarggarer 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 GITCITICCCAITGICAGAGCICAGAGCICTCCAGATTAIACCCCAGAGGCGCAGATTIAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
1, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Bmail: romieu@ensam.inra.fr
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                            CTTGAGTCCAAATAT 619
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/Globella Seeds / Callected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. CDNA was prepared from polyanciched RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Giapaex III Gold packaging extracts. Plasmids containing containing misers were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
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                                                                                                                                                             /tissue_type="lmmature seeds"
/dev stage="Immature seeds, 11 to 19 days after
pollination"
/clone_lib="GESD"
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0; Mismatches 154; Indels
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                                                               /organism="Medicago truncatula"
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/clone="pGBSD9J4"
                                                                                /mol_type="mRNA"
/cultivar="A17"
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al Similarity 71.8%;
407; Conservative
          Seg primer:
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Unpublished (2001)
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                                                                      62 ACTGCGAAACTGGGCTTGCTCACTCTTCATTCTAATAACATCAAGAAATTCCCT
                                                                                                              28 ATTGCGAAACCGAACGTTTCAATTTTCATATCAATGAAACTCAATTTCCT
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Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T.,
Cho, J. and Fraser, C.M.
                               Gaps
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              Pred. No. 2.5e-37;
0; Mismatches 154; Indels
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1100 Bates Street, Houston, TX 77030-2600, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
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Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
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            1 Similarity 71.8%; 407; Conservative
              Local Similarity
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Medicago.

18 (bases 1 to 612)

19 Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)

10 Contact: Dixon RA Plant Biology Division

11 The Samuel Roberts Noble Foundation

12 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7300

12 Fax: 580 221 7300

12 Fax: 580 221 7380

13 Fax: 580 221 7380

14 Email: radixon@noble.org

15 Insert Length: 512 Std Error: 0.00

16 Plate: 036 row: F column: 08

17 Seg primer: TCACACAGGGGTAATGAC.
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/dev stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF645522 612 bp mRNA linear EST 20-DEC-2000 NF036F08EC1F1074 Elicited cell culture Medicago truncatula cDNA clone NF036F08EC 5', mRNA sequence.
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Medicago truncatula
Medicago truncatula
Medicago truncatula
Sukaryota, Viridiplantaen; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                            GAAGACAAGTITGITGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAAGACCAGGTTGAG 481
                                                                                                                                                                                   414 GRAGACATTITIGITIGCCRARGITRARATIGGAATAGIGGIGARARAGACCRGGITIGAG 355
                                                                                                                                                                                                                                             482 GATGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGATTGGAGACGGCAAGATT 541
                                                            474 GTCAAGGGGTTTGGTGCTCAGGTGGCTCAAAAGAGAGGCAGGGAGGCTCCGAATTTTCT
                                                                                                                                                                                                                                                                                                 354 GCAGTGATAAACAAAATTATGGAGACGCCAAGAACTGGGGAGATTGGTGATGGCAAAATT
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/organism="Medicago truncatula"
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/db_xref="taxon:3880"
/clone="NF036F08EC"
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Best Local Similarity 70.9
Matches 402; Conservative
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratugene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
                  CA922829 812 bp mRNA linear EST 09-MAY-2003
EST640547 MTUS Medicago truncatula cDNA clone MTUS-58H7, mRNA
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                                                                                                                                                                                         Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Sukaryota, Viridiplantaei, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                               Vandenbosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.

The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries
Unpublished (2002)

Contact: Vandenbosch K
Department of Plant Biology
University of Minnesote K
University of Minnesote K
220 BioSci Center, 1445 Gottner Ave, St. Paul, MN 55108, USA
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33.1%; Score 297; DB 14; Length 812;
Best Local Similarity 71.6%; Pred. No. 3.6e-37;
Matches 406; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kvandenb@cbs.umn.edu
Alias Clone pWHRP-28F3
TIGR sequence name: MTUCF91TV
More information is available at: www.medicago.org
Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
1. ostion/Qualifiers
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/tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_nost="XLOLR"
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/cultivar="A17"
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CA922829.1 GI:27409759
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Fax: 612 625 1738
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Omura, M.
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Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
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                         44 ATTGCGAAACCGAACGTGTTCAACGGTTTGAATTTTCATATCAATGAAACTCAATTTCCT 103
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                                                                                                          182 ACCGCGGTCAAGCGTAAGATATGCCCCCCGTCGTTCCTGTGATTAATGCCCAAAGCTCG
                                                                                                                               CCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCTGGCGA
library
Inpublished (2003)
Contract: Gary Stacey
University of Missouri
IOB Waters Hall, Columbia, MO 65211, USA
TH: 573-884-4752
Fax: 573-882-0588
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/mol type="mRNA"
/cultivar="Williams 82"
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Makaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosida II, Sapindales; Rutaceae; Citrus.
1 (bases 1 to 866)
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gmrhkww3"
                                                                                                  /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA c generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
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Contact: Mitsuo Omura
                                                                                                                                                                                                                                                    Length 759;
                                                                                                                                                                                                                                                 31.7%; Score 284.2; DB 14; Length ilarity 72.7%; Pred. No. 3.8e-35; Conservative 0; Mismatches 138; Indels
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National Institute of Fruit Tree Science, Okitsu
Okitsu 485-6, Shimizu, Shizuoka 424-0292, Japan
Tel: 81-543-69-7108
Fax: +81-543-69-2115
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GI:10255665

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BE823431.1
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COMMENT
VERSION
KEYWORDS
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                                                                                                                /db_xref="taxon:55188"
/clone="pcMFrMO1.17-061"
/tissue type="juice sac and pulp segment"
/dev_stage="maturation stage"
/clone lib="Citrus unshiu juice sac and pulp segment
maturation stage"
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                          8 COGCCOCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAG
                                                                                                                                                                                                                                                                31.5%; Score 283; DB 13; Length 866; 71.8%; Pred. No. 5.3e-35; ive 0; Mismatches 143; Indels 4
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                                                            /organism="Citrus unshiu"
       Email: xx145039@affrc.go.jp.
Location/Qualifiers
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BB823431 Gm-r1070 Glycine max cDNA clone Gm-r1070-7536 3',

mRNA sequence. BE823431

ACCESSION

LOCUS DEFINITION

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Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, University of Illinois, http://www.lincedh/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /done="dm-dx001304f"
/clone="fm-dx001304f"
/clone=|The library Gm-r1070 is a sequence-driven, reracked fore rithe library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 represent 2,639 sequences from immature cotyledons, 1,770 represent 1,639 sequences from immature seed coats, 3,938 from flowers, and 869 from young pode. The 5' ESTS of the source clones from the different libraries was used to select singletons, or a representative of each conting, which were reracked con library Gm-ri070. The cDNA clones of the reracked Gm-ri070 library were then sequenced at the 3' end. The conting analysis to select unique genes was performed by the laboratory of Ennest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.com.edu/ResearchProjects/Soybean/index.html
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                                                                                                                                                                                                                                               Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H. A Functional Genomics Program for Soybean (NSF 9872565) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: Genome Systems, Inc. 4633 World barkway Circle &t. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or ontact:clones@genomesystems.com or info@genome
                                                          Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewin, H. A., Director, Keck Center for Comparative and Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
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Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
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Best Local Similarity 72.2%; Pred. No. 4e-34;
Matches 345; Conservative 0; Mismatches 133; Indels 0:
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Seq primer: 5'-TTTTTTTTTTTTTT(A/C/G)-3'
Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:3847"
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Glycine max (soybean)
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1 (bases 1 to 677)
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                               Glycine max
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; laminids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 711)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
van der Hoeven, R.S., Romning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                       165 crańcecearrarcagadercaaacerecedarritegiedegegiedaaaaritrada 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGAGGCAGGCGGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGG
                                                                                                                                                                               213 TCGTTCCTGTGATTAATGCCCAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACA
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Bmail: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
  Length 799;
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/mol_type="mRNA"
                                                   155;
Score 276; DB 12;
Pred. No. 6.9e-34;
0; Mismatches 155;
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       30.8%;
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Unpublished (2001)
       Query Match 30.8
Best Local Similarity 70.4
Matches 369; Conservative
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute Orders can be made through URL:
http://genome.arizona.edu/orders/
Seg primer: T3.
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Van der Hoeven, S. Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,
Tanksley, S. and Baker, B.
Unpublished (2001)
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                                                        373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 AAAATCATTGAGGAAGGCAAGAACTGGAGAGATTGGAGACGGCAAGATTTCTTGCTGCT
                                                                                                                                                                               GGTGCTCAGGGTGGTTCAAAAGAGGGCAGGAGGCTCCGAATTTTCAGAAGACAATTTT
                                                                                                  555 TCTGCGGCTTTGTTGAAAATGGGAATTCGTGGTGTCACTGTATCTGATGTCAGGGGCTTT
                                                                                                                                            GSTSCTCAAGGTGGTTCAACTGAGAGGCAGGGCGGCTCAGAATTTTCTGAAGACAAGTTT
                                                        TCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTCTGATGTTCGAGGTTTT
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/dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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9712 Medical Center Dr, Rockville, MD 20850,
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/clone="cPRO18M20"
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/cultivar="Kennebec"
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EST281945 tomato callus,
cLEC36D8, mRNA sequence.
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                   /db_xref="taxon:4081"
/clone="cTGCZ2H10"
/tissue_type="flower"
/dev stage="buds 8mm to preanthesis"
/dev stage="buds 8mm to preanthesis"
/dev stage="buds 6mm to preanthesis buds
/clone lib="tomato flower, 8 mm to preanthesis buds
/clone lib="tomato flower, 8 mm to preanthesis buds
/note="vercor: pBluescript SK(-); Site_1: BCoRI; Site_2:
Xhof; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
vere taxen from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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AJ558383.1 GI:31660955
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Antirrhinum majus
Antirrhinum majus
Bukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots;
asterids; lamids; Lamiales; Antirrhinaceae; Antirrhineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 AGACACGITIGITIGCAAAAGTIAAAATIGGAAATTGITGICAGCAAAGACCAGGITGAAGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGGCGGGGTGATAAGGCTGA 603
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Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
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                                                                                                                                                                                                                                                                                         Score 275.8; DB 12; Length 711;
Pred. No. 8e-34;
0; Mismatches 127; Indels 0;
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Carl-von-Linne Weg 10, D-50829, Germany
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Molekulare Pflanzengenetik
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Unpublished (2003)
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.5%;
Matches 352; Conservative (
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613 bp mRNA linear EST 18-MAY-2001
TAMU Lycopersicon esculentum cDNA clone
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 GAAAGACAGTTTGGCTCTGAATTCTCAGAAGACAATTTTGTTGCAAAAGTTAAGATGGAG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 GGTATTCGAGGTGTTACTGTTTCTGATGTTTGGTGCTTCAAGGTGGTTCAACT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 GAGAGGCAGGCGCCCCCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAAGTTAAGATGGAG 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 ddaairicgredichchchchchcharchacdadderringerrchchaddadharaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                      169 gerecearrerragssereagarrrerecagareceracergaereceaagrreracaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 ACTGGAGAGATTGGAGGCGAAGATTTTCTTGCTGCTGTTTCAGATGTAAGAGTC
                                                                                                                                                                                                                                                                                                                                                                              GITCCTGTGATTAATGCCCCAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAA
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                                                                                                                                                                                                                                                    Length 732
                          /mol_type="mRNA"
/db_xref="taxon:4151"
/db_ore="la18 1 07 f22"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                               95; Indels
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8%; Pred. No. 1.1e-33;
Matches 332; Conservative 0; Mismatches 95.
/organism="Antirrhinum majus"
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cch completed: May 28, 2004, 00:14:53
time : 2080.03 secs
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                                                                                                                                                                                        /clone lib-*tomato callus, TAMU*
//clone lib-*tomato callus, TAMU*
//note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; supplier: Giovannoni laboratory; GLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. [ (bases I to 648)  
D' Ascenzo,M., He,K., Lyman,J., Matern,A.L., Vision,T., Holt,I.E. Liang,F., Joton,J., Ronning,C.M., Craven,M.B., Fulii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 TCAACAGGTTTCTTCGGCACTACTGAAAATGGGCATTCGTGGTGTCACTGTTTCGGATGT
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0
                                                                                                                                                                                                                                                                                                                                                                              Length 613;
                                                                                                                                                                                                                                                                                                                                                                          Score 274.2; DB 9; Length
Pred. No. 1.6e-33;
0; Mismatches 128; Indels
                             /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                    /dev stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
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                                                                                           /db_xref="taxon:4081"
                                                                                                                                   /tissue_type="callus"
                                                                                                              /clone="clEC36D8"
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llarity 73.3%;
Conservative (
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Matches 351; Conser
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                                                                                                                                                                                                                                                                                          x Money Maker)*
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="tomato resistant, Cornell" /clone lib="tomato resistant, Site 1: EcoRl, Site 2: /note="Vector: pBlueScript SK(-); Site 1: EcoRl, Site 2: Xhol; cLER - Tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRl and 3' end with Xhol site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGGTCAAGCGCGTAAGATATGCCCCCCGGTCGTTCCTGTGATTAATGCCCCAAAGCTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 CICGCAAGITICCICGGCTITGCIAAAATTGGIATTCGAGGTGTIACTGTTTCTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGAGGTTTTGGTGCTCAAGGTGGTTCAACTGAGAGGCAGGGCGGCTCAGAATTTTCTGA
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0
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudornas resistant tomato
Unpublished (1999)
Contact: CVGI
Clemson University
Clemson University
Clemson University
LD Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 648;
                                                                                                                                                                                                                                                    /organiem="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="R11-12 (35S::Pto in Rio Grande
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/dev stage="4-week old"
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Best Local Similarity 75.74;
Matches 339; Conservative (
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compuger Ltd.
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1 (bases 1 to 588)

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Patent: US 6177275-A 15 23-JAN-2001;
Location/Qualifiers

PAT: 16-MAY-2001

linear

DNA

ALIGNMENTS

Sequence 15 from patent US 6177275.

AR125591.1 GI:14111653

Unknown. Unknown.

X97496 Synechocyst D90915 Synechocyst AP004597 Oceanobac

D90915 AP004597 AP005341

4.4.886.23 4.4.86.23 8.5.23 8.5.23

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AR376903 Sequence

AJ489604 Pinus pin AC007138 Arabidops AL161493 Arabidops AK0668407 Oryza sat AK099152 Oryza sat X97377 F.diplosiph AB077165 Prochloro AF022186 Cyanidium AF017419 Nostco pu MG447 Synechococc AL771089 Prochloro AL800674 Aquifex a BK572099 Prochloro AP06568 Gloeobact AP06568 Gloeobact AP06568 Gloeobact AF06591 Vibrio pa AE016803 Vibrio vu AR408756 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AK067460 Sequence AJ251822 Anabaena AP003589 Nostoc sp BX572094 Prochloro U38804 Forphyra pu Sequence Ricinus c Sequence Sequence Arabidops Medicago Lycopersi Synechoco AR125591 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AY027892 | AY442185 | AF095455 AF079137 SUMMARIES SYOGLNB PMA271089 AE000674 PPI489604 AC007138 ATCHRIV5 AK068407 AK099152 FDGLNBPRT AE017165 AP003589 BX572094 PPU38804 AF079137 AR095455 AR125592 AR095454 AR125590 AY027892 AE016803 AR408756 AP005340 BX572099 AR125589 AY442185 AP005370 AP005081 BB 100.0 48.5 48.5 48.5 48.5 48.5 48.5 48.5 48.5 88.4 48.5 88.6 88.7 41.7 98.7 Length Query 95.8 95.8 94.2 285 250.8 245 209.6 1999.8 1199.8 4.109.4 109.8 4.701 8.601.8 102 101.6 98.6 94 93.6 Score Result No. υ

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/db_xref="taxon:3702"
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 2133 28-FBB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)
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/mol_type="unassigned DNA"
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/crganism="unknown"
/mol_type="unassigned DNA"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II: Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 591)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, J., Carninci, P.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
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Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Carninci,P.,
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                                                             301 GITACTGITICICALGROAGAGITIGGIGCACAAGGAGGITCTACCGAGAGACACGT
                                                                                                                                              361 GGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAG
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100.0%; Pred. No. 2.7e-137;
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nirrogen regulatory P-PII genes
Patent: US 6177275-A 13 23-JAN-2001;
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/mol_type="unassigned DNA"
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Sequence 13 from patent US
AR125589
AR125589.1 GI:14111651
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Matches 588; Conservative
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/db_xref="G1:28950699"
/translation="MAASHYRPISITSLGFYSDRKNIAFSDCISICSGFRHSRPSCLD
LyrgsPSNNSRVLPVVSAQISDYIPDSKFYKVEAIVRPWRIQVSSALLKIGIRGVT
VSDVRGFGAGGGSFRHGSEFSBDKFVAKVGMBIVVKKDQVBSVIRTIIBGARTGBI
GDGKIFVLPVSDVIRVRTGBRGEKAEKAMTGDMLSPS"
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Ism, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Ecker, J.R.
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                                                                                                                                                                       Direct Submission
Submitted (14-MAR-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AAGAACATTGCTTTCTCTGATTGCATTTCGATTTCTGGATTCAGACATTCCCGACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim,C.J., Chen,H., Chenk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
                                                                                                                                                                                                                                                                              RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN crabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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/db_xref="taxon:3702"
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/clone="U23463"
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Best Local S:
Matches 588
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                                                                                                                                                                                                                                                                                                                                                                             GGTGATGGCAAGATTTTTGTTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                             GGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAG
                                                                                                                                                                                                                                                                     GECTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATTGTTAAG
                                                                                                                                                                                                                                                                                                                                151 TCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTT
                                 AGTGCCCAAATATCTTCTGATTATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATT
                                                   211 AGIGCCCAAAIAICTICTGAITATAITCCCAGACTCGAAAITITACAAGGGGAAGCAAIT
                                                                                                   GTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGT
                                                                                                                                 GTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGGTTCGAGGT
                                                                                                                                                                                                                                                                                                           421 AAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGTT
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Pred. No. 4.8e-61;
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
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/wol_type="unassigned DNA"
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Sequence 16 from patent US 6177275.
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Patent: US 6177275-A 16 23-JAM-2
Location/Qualifiers
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al Similarity 70.3%;
397; Conservative
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LVTXSPSNNSRVLPVVSAQISSDYIPDSKFYKVBAIVRPWRIQQVSSALLKIGIRGVT
VSDVRGFGAQGGSTERHGGSSFSEDKFVAKVRMEIVVKKDQVESVINTIIEGARTGEI
GDGKIFVLPVSDVIRVRTGERGEKAEKMTGDMLSPS"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                          AAAGACCAAGIGGAATCTGTAATCAACAAAAAAAGAGCAAGGAGCAAGGAGAATT
                                                                          453 AAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATT
                                                                                                              GGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAG
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Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.M.
Direct Submission
Submitted (29-SEP-1998) Biology, New York University, 100
Washington Square East, New York, NY 10003, USA
Location/Qualifiers
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/function="putative role in nitrogen eensing"
/note="GLB1"
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/protein_id="AAC78333_1"
/db_xref="GI:3885943"
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/map="10.8 cM"
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             67 ATTGCTTTCTCTGATTGCATTTGGATTTGTATTCAGACATTCCCGACCATCTTGC 126
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Coruzzi, G. M., Lam, H.-M. and Hsieh, M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 14 23-JAN-2001;
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Sequence 14 from patent US 6177275.
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ykkuykapyvpvinakospyviplakerykvakilrpmkvsovsbalikigirgvyvs
dvrgepaqogosterogosrpspprvakvkmeivvskoovpoviekiibrarygeigd
gkifildpvsdvirvrtgergdkaermyggrsdms"
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Ricinus communis
Rukaryota, Viridiplantaen; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
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                                                                     Grircicarstrocadgrirringerectcaaggregircaacrdagaggcaggegerea 363
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CCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACT 303
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                                                                                                                                                                                                              CAGGITGAGGAIGITAIAGAAAAAAICAITGAGGAGGCAAGAACTGGAGAGAITGAGACC
                                                                                                                                                                                                                                                                                  GTTTCTGATGTGAGAGGGTTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCT
                                                                                                            GASTICTCGGAAGACAAATTIGTIGCTAAAGTTAAGAIGGAAAICGTTAAGAAAGAC
                                                                                                                                 GGCAAGATTTTTGTTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAAGGTGAGCGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acalypheae; Ricinus.
1 (bases it to 840)
Hsich, M.H., Lam, H.M., van de Loo, F.J. and Cornzzi, G.
A PII-like protein in Arabidopsis: putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 840)
Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M.
Hsiect Submission
Submitted (29-SEP-1998) Biology, New York University, 100
Washington Square East, New York, NY 10003, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Matl. Acad. Sci. U.S.A. 95 (23), 13965-13970 (1998)
99030678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear
partial cds.
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/mol_type="mRNA"
/db_xref="taxon:3988"
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/protein id="AAC7832.1*
/db xref="GI:3885941"
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KGFCAQGGSKERQGGSEFSEDNFVAKVKMEIVVRKDQVEAVINKIMETARIGEIGDGK
IFLIPVSDVIRIRTGERGEQAERMAGGLTDALXV"
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Submitted (22-FRB-2001) Molecular Biology Program, New Mexico State
University, Corner of Knox and College, Las Cruces, NM B8003, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAK16221.1"
/db_xref="GI:13277515"
/translation="MTLIAXPNVFNGLNFNINETQIPFSSFSVIRKRFGDSSHRNVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA linear PLN 12-MAR-2001 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                     GITTCTGATGTGAGAGGTTTTGGTGCACAAGGAGGTTCTACCGAGAGACACACGGTGGCTCT 366
                                                                                                                                                dirrichdahdrucdaddruringgrechcaadgredrifdaacreaddaddeddeddedda 412
                246
                                GAGTICICGGAAGACAAATTIGIIGCTAAAGTIAAGAIGGAAAICGIIGITAAGAAAGAC 426
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                                                                                                                                                                                                                                                                                    GGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGCGTGGG
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                                                                    TACTGAAAATCGGGATTCGAGGTGTTACT
                CAAATATCTTCTGATTATATCCAGACTCGAAATTTTACAAGGTGGAAGCAAT
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Garcia-Ibilcieta, D. and Sengupta-Gopalan, C.
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(GLNB) in alfalfa
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/organism="Medicago sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                AY027892 796 bp
Medicago sativa PII protein (GLNB)
AY027892
                                                                      CCATGGAGATCCAGCAAGTTTCATCGGCTT
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/db_xref="taxon:3879"
                                                                                                                                                                                                                                                                                                                                                                  GATAAGGCTGAGAGGATGACAGGAG
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Characterization of PII
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'product="PII_
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/gene="GLNB"
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Score 250.8; DB 8; Length 796; Pred. No. 1.9e-52;

42.78; 76.18;

Query Match Best Local Similarity

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/translation="MASPSLSKSNFSLHSFSSSPSLSQFPHFTSITVVQPKFFPSQLTFKCOMBSPSTITANOPKFFPSQLTFKCOMBSPSTITANONSPDFYPDAKFYKVEAILRPWRIQQVSSALLKMGIRGVTVSDVRGFGAQGGLTERQAGSEFSEDTFVAKVKMEIVVSKDQVBGVIAKIIEEARTGEIGDGKIFLTPISDVIRVRTGERGEKAERMMGGHADMSSALSTS"
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Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Subraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
225
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                                                                                                                                                                                                                             ATCGGGATTCGAGGTGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCT 345
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                                                         GITCITCCCAAAATTAGAGCTCAAAACCTTCCTGACTATGTTCCTGAATCCAAGTTTTAC
                                                                                                                                                                                                                                                                                                                                                 ACCGAGAGACACGGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATG
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GITITIACCTGTCGTTIAGTGCCCAAATATCTTCTGATTATATTCCAGACTCGAAATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AGGACAGGAGATTGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGA
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Stuttgart 70593, Germany
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/mol_type="mRNA"
/db_xref="taxon:4081"
1. -947
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Walch-Liu, P., Roemheld, V. and von Wiren, N. Direct Submission
Submitted (17-0CT-2003) Institute of Plant University, Fruwirthstr. 20, Stuttgart 7059
Location/Qualifiers
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Walch-Liu, P., Roemheld, V. and von Wiren, N. A PII-like protein in tomato
Unpublished
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/db_xref="GI:38231570"
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Gaps

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us-09-756-541-15.rge

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Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence.
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1 (bases 1 to 120185)
Huang,E.N., Mascimento,L., de la Bastide,M., Habermann,K., Vil,M.D., Preston,R.R., Spiegel,L.A., See,L.H., Shah,R., Matero,A., O'Shaughnessy,A., Rodriguez,M., Shekher,M., Swaby,I., Schutz,K., Arabidopsis thaliana BAC T7B11 from chrocosome IV near 10 cM Unpublished
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Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
          /translation="MAAHLPDFVKGSIFSLPSSTSTSSSCTYSSISHTAASPGFHSSP
AAAKKSVK.GTMGRNGSVRSVKHRYTSLHAKNEKRQQIKASAGABVGTNTHPDTVPEA
RYKVBAILRPWRISHVTTGLLKMGTRGVTVSDVRGFGVQAGSAERQAGSEFSKDNFV
SKYKKRITVKSKDQYBAXIDALIDEARTGEIGDGKIFVVPVADVIRVRTGRRDLKPERM
AGGDQRYLQVYIKRLQTATKSLLAL"
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                                                                                                                                                     Length 1085;
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                                                                                                                                                         DB 8;
                                                                                                                                                         Score 209.6; DB 8 Pred. No. 4.3e-42;
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Parnell, L.D.
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70.9%;
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Submitted (11-JUN-2002) Canton F.J., Molecular Biology and
Biochemistry, Faculty of Sciences, Campus de Teatinos s/n, E-29071,
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Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus.
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478 AGGAGTCATTGCCAAGATAATTGAAGAGCAAGAACTGGTGAAATAGSTGATGGAAAGAT
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                                          Gape
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A PII-like protein from xylem of adult Maritime pine trees Unpublished
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/function="putative nitrogen sensor protein"
Length 947;
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Score 245; DB 8; Length 94
Pred. No. 5.4e-51;
0; Mismatches 120; Indels
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/protein_id="CAD33967.1"
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|mol_type="mRNA"
|db_xref="taxon:71647"
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1. .1085
/gene="glb"
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glb gene, PII-like protein.
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  Query Match
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Matches 317; Conservative (
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/evidence=not_experimental
join(10826. 10842,10929. 11371,11559. 11770,11843. 12130,
12260. 12433,12526. 12762)
/gene="T7811.4"
/note="identical to T15816.7, GenBank accession numer
API04919; functional catalog ID=99"
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LRDBYILRGIANGLLFDKAYRVDGHGKKDMMKKOGPKLGLYGWIAGADDYNVDGREGE
ESAKLNAIQERTMRHIQKIVDDHERLTKLLESEKKKLEIKGNELAKPOVHNOTERMKL
SEDLEQRQKEELHEKIIRLERQIDQVQAIBLEVBQLKGQLNVMKHMADDGDAQVVKEV
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SKLSNVNSLPEKIWLKKQIAIGINEVTRVLERMNPNNTSDQQQNPKQLQVVILVADCK
PRMLTKHIPNLAASRNVPVLYVRDNKRASLRLGELVKLKTALAIGIKARGNDLMLLK
                                                                                                                                                                                                                                                                                                        /db_xref="GI:4558547"
/translation="MGGTRHCYGLGYEMFNPVWSSSVRFVWSSSSTLFKIVIITRSLC
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OOKY OOBDVEDRAVEVLOLMERY INDPDMHPYKRVKLENODREVEVIDDRDEKLRELK
ADLGDGPYNAVTKALLEINEYNPSGRY ITTELMNFKEDKRATLERGVTCLLDOMEKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="encodes hypothetical protein; identical to
TISB16.7, GenBank accession number AF104919; gene model
                                                                         number AF104919; gene model
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                                                                                                                                                              .9778,9900. .10112}
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/note="encodes RNaseP-associated protein; identical
                                                identical to
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product="putative RNaseP-associated protein"
                                                      protein;
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join(8080, .8568,9318. .9479,9557.
/gene="T7811.3"
/note="identical to T15816.8, GenBa.
AF104919; similar to T7811.1; funct
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/product="hypOthetical_protein"
/protein_id="AAD22640.1"
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                                                /note="encodes hypothetical
T15816.8, GenBank accession
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/db_xref="GI:4558548"
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                     gene="T7B11.3"
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/gene="T7B11.2"
/note="identical to T15B16.6, GenBank accession number
AF104919, similar to A. thaliana CHP-rich proteins encodes
by T10M13, GenBank accession number AF001308; functional
catalog ID=98"
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EVCSGCNERSYHVLRCIEDNGGFILDFGCATFPQVVKHRIEDQPLSLCYGEKASGKYW
CDICEKETNPNTWFYTCKDHRASLHTWCVLGDFWGLIPKSTIELMNISYEVVLNNSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tränglation="MOSDGVSVPLTHEHLAMPCNDLRRGDCCERLEAISDGYYCTTCD
PFVHKKCGDEASECIENPFHSNHPLRLGFLSRLQRQHMLKVVRSCDLCGKNIGDLFYR
CEICDFDMDLHCAKYPPLEVIDIPEMHSHKLNLLKDRVBFDCDAKCGKIGYGFPYECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOSKPHYDCYRYSSSEBVKHPLEYNHSYHSLHPLKLLAGQPPDYSDGKCRLCGRKID
DKLPYHCSSCNPTLDMRCYLNPPPKSYLDLKTHDHQLNLLPRLIFFTCNACGLNGDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAQKQQTLHQQRPFSSSPRSYSSISNRPIFLLSRNGLLLVLAL
FLLLGVFLPWPGSPLLLFPNKVSSPSYASSLSPHAKSFWRNYTLAQAAKFVATNGTV1
VCAVSSPFLPFLNNWLISVSRQKHQEKVLVIAEDYITLYKVNEKWPGHAVLIPPALDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIAYSEGSQFFNFTARRDQHLLQILELGYNWYNDUMVWLQDPFQYLBGSHDAYFT
DDMPQIKPLAHSHDLPAPDQWSTYICSCMIYLRPTWGAKLLMKKWSEBLQSQAWSES
TRIGNDDAPRULALMKTAHQVDLYLLSQVAPPTGGLYFNDAMWKETKGKHVIVHNN
YIIGYDRKMRRPQDVCIMLVDDHALESPLGKLQ"

COMPLEMENT (2647. 4650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYACFQCDFLIHKDCFGLPRLININRHDHRISRTSLIGIVNSVCGVCRQKVD#TCGGY
SCQRCSTYIAHSKCATREDV#NGKELEGVPEEIEDIEPYVVIDDNTIQHFSHKEHYMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINVNGLMCEVNKRCNACNHPISPQSFYGCMDCDFILHQNCAGFPRRKWHVLHNERLAL
                              1 Bungtown Road, Cold Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="encodes putative CHP-rich zinc finger protein; identical to T15B16.6, GenBank accession number AF104919; gene model last edited on 3 Mar 99"
                                                                         Arabidopsis trialiana BAC T7B11 from chromosome IV near 9.5 cM The T7 end of T7B11 is oriented toward the NOR and overlaps with T15B16, GenBank accession number AF104919. The SP6 end of T7B11 is oriented toward the centromere and overlaps with T10M13, GenBank accession number AF001308. There are no discrepancies found in these independently finished overlaps. The region from position 110064 to 110253 exists as single stranded and single chemistry. Please see the feature below for details.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number AF104919; gene model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF104919; similar to T7B11.3; functional catalog ID=99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="T7B11.1"
/note="identical to T15B16.9, GenBank accession number
         Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="overlap with T15B16, GenBank accession number AF104919, from position 1 to 14923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
join(50. .556,1098. .1259,1340. .1561,1668. .1880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; identical to
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/product="putative CHP-rich zinc finger protein"
/protein_id="AAD22638.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPICRHCKSHCIPPIILKKIGTSDPYFCSLDCIBSFKRLWRAK"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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                                    Center, Cold Spring Harbor Laboratory,
Harbor, NY 11724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="T7B11.1"
/note="encodes hypothetical
T15B16.9, GenBank accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="near 10 cM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="T7B11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome="IV"
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FEATURES

REMARK

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/ Godon start=1
/ produCt="putative protein transport factor"
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EFRFPAPRILAFKBARFPQIRTLITTEQRMKLKSSFIEFDEASFCEWMRSLKVVPPEPR
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.14198))
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV4 at the 5' end and an overlap with ATCHRIV6 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similarity to
contains EST gb:H36218, AA651596, T42768, AI997386.1,
                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (5603. .5740,6062. .6178,6259. .8079,8177. .8671))
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.13904,13995.
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/gene="AT4g01820"
complement (join/9603. .9956,10053.
10835. 11101,11218. 12029,12106.
13293. 13514,13592. 13767,13850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5740,6062.
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/variety="Columbia"
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/number-
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8177. .8671))
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                                                                                                                                                                 Location/Qualifiers
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/gene="AT4g01810"
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                                                                                                                                                                    FEATURES
            COMMENT
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QVPRFLGLKVGLIQQNMTPEQRKENYLCDITYVTNSELGFDYLRDNIATESVBEIJULR
DENYCYIDEWOSILIDBARTPLIISGPAEXPSDQYYKAAKIASAPERDIHYTVDEKQK
TVLTRQQYEDAERILUDVLYDPERQMSYVLNAIKAKELFLRDNYYIIRAKGKIND
DEFTGRYMQARRWSGGLAQAYEAKEGLEIQNESITLASISYQNFLQPPKLCGMTGTA
STESAEFESIYKLKVTIVPTNKPMIRKOBSDVVFKANNGKWRAVVVEISRMHKTGRAV
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                                                                                                                                                                                                                                                                 'codon start=1
'evidence=not_experimental
'product="putative SecA-type chloroplast protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MYSPLCDSQLLYHRPSISPTASQFVIADGIILKQNRLLSSSSFW
GTKFCNTVKLGVSGCSSCSRKRSTSVNASLGGILSGIFKGSDNGESTRQQYASIVASV
NRLETBISALSDSELRERTDALKQRAQKGBSMDSLLFFAFAVVREASKRVLGLRPFDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAACATTGCTTTCTCTGATTTGCATTTGGTTTCTGGATTCCAGACATTCCCGACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, B-mail: lemcke@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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Spiegel, L.A., Huang, E.N., Nascimento, L.U., de la Bastide, M.,
Yreston, R.R., Matero, A., Shah, R., O'Shaughnessy, A.,
Rodriguez, M., Shakker, M., Schutz, K., See, L.H., Swaby, I.,
Habermann, K., Dedhia, N.N., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
   15196. .15263,15359. .15510,15686. .15787,15883. .15946,
16035. .16134,16215. .16361,16449. .16515,16710. .16885,
17107. .17274,17533. .17646,17718. .17831,17987. .18205,
18310. .18488,18577. .18684,18783. .18989,19082. .19154,
                                                                                                                                                                                                    fnote="functional catalog ID=06.04; functional catalog
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Arabidopsis thaliana
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EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                            'protein id="AAD22642.1*
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                                                                                                                                                                              gene="T7B11.6"
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AL161493.2 GI:7268564
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Matches 201;
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TITLE
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ATCHRIV5
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50605 ATGSCGGCGTCATGACGAAACCCATCTCATAACTTCTCTCGGTTTCTATTCTGATCGA 50664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soss aagaacarrecriterergarrecarrecarrecriterrergaarreagacarrecegacea 50724
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Oryza sativa (japonica cultivar-group) cDNA clone:J013149B08, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14552. .19316
| Game="AR4901830"
| Complement(joi30" | 14905,14994. .15290,15475. .15738,
| 15809. .16075,16311. .17110,17180. .17979,18068. .18306,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AAGAACATIGCTTICICIGATIGCAITICGAITIGTICIGGAITCAGACAITCCCGACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTT 180
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AIGGCGGCGTCAAIGACGAAACCCAICICAAIAACIICICCGGGIIICIAIICIGAICGA
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llarity 99.0%; Pred. No. 8.4e-40;
Conservative 0; Mismatches 2.
                                                                                                                                                                                                           .13767)
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                                                                                                                                                                                                                                                                      complement (13768. . /
/gene="AT4g01820"
/number=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (13995.
/gene="AT4g01820"
               complement (13226.
                                                                                                                                                                                                                                                                                                                                            complement (13850.
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/gene="AT4901820"
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AK068407
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                                                                                                                                                                                                                                                                             /translation="MEEKTKYVPFYALESFSDSTDVLMIVGSIGAIGNGVGFPLMTL
LFGDLIDSIGQNGSNKDIVEIVSKVCLKFVYLGLGTLGAAFLQVACMYTGERQAARI
SEYLKKTILIGQDIGFPDVETSYGEVVGRNSGDFVLLIEBAMGEKVGKFLQLIATFVGGR
NLAFKGMLLILVAN VS IPLIAGAAMPIITYRASSREQAAYAKASTVVEQTLGSIR
TVASFTGEKQAMKSYREFINLAYRASVKQGFSMGLGIGVVFFVFFCSYALAIMFGGBM
ILKKGYTGGEVNNWYTVASSNSLGGTTPCLITAFAAGRAAAKNMFETIBRKSIDAF
DLNGKVLEDIRGEIBLADVCFSYPARPMETVGFSTLLIPSGATAALVGBSGGGKSSY
ISLIERFYDPSSGSVLDGVNLIGGNIKRIGKTGLVSGRPTLYGGGKSSY
ATVEELQAAKLANAARIIDKLRGGIGFTLYGENGTQLGGGGKRAANAKHETIOFDRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLGILGROENTEISRROSRRNSITRIAALNKPETTILILGTLLGAVNGTIPPIFGIL
PAKVIEAFFKPPHDMKRDSRFWSMIFVLGVASLIVYPMHTYLFAVAGGRLIQRIKW
CFEKVVHMEVGWFDDPENSSGTIGSRLSADAALIKTIVGDSLSLSVKRAAAVSGILI
ASTASWKLAVIILWIIPLIGINGYLQIKPIKGFTADAKAKKTEASQVANDAVGSIRTV
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SGLVLENVKGDIELCHISFTYQTRPDVQIFRDLCFAIRAGGTVALVGESGSGKGTVIS
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SABREILAARLANAHGEISSLQQGYDTVVGBRGIQLGGGQKQRVAIARAIVKBPKIL
LLDBATSALDARSBRVQDALDRWYNRTTVVVAHRLSTIKKADVIAVKNGVIVBKG
THETLINIEGGVYASLVQLHISASS"
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SHSELLKDHEGAYAQLIRLQKIKKEPKRLBSSNELRDRSINRGSSRNIKTRVHDDDSV
13835. .11:01,11218. .12029,12106. .12905,12987. .13225,
13293. .13514,13592. .13767,13850. .13904,13995. .14198))
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/note="evidence: experimental, likely to be involved in
                                                                                          lipophilic transport
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R90081, AA605450"
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/gene="AT4g01826"
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/numher-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (9603. .9956)
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/gene="AT4g01820"
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/gene="AT4g01820"
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/gene="AT4g01820"
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PUBMED REFERENCE

AUTHORS

JOURNAL MEDIINE

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fulanda, S., Hanagaki, T., Hara, A., Hashizume, M., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayashizaki, Y., Hayasusu, N., Hiramura, K., Hayashida, Y., Iida, Y., Iida, Y., Ishikawa, M., Iroh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kayamata, M., Kahikawa, M., Iroh, M., Kodama, T., Kojima, K., Kojima, K., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Miura, J., Miyazaki, M., Masuda, H., Matsuyama, T., Miura, J., Miyazaki, M., Masuda, H., Marakami, K., Matsuyama, T., Miura, J., Miyazaki, M., Marikami, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Marikawa, K., Mikura, J., Nishi, K., Nomura, K., Oataco, N., Ota, V., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sasaki, M., Sano, H., Sasaki, D., Satoh, K., Sagabo, Y., Sugano, S., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugano, S., Toya, T., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Waki, K., Xie, Q., Yahagi, W., Anada, H., Yamamoto, M., Waki, K., Xie, Q., Yahagi, W., Anada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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Fals Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fuls Genome Sequencing & Analysis Group: Otomo, Y., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Muraa, J.,
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Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
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Yasunishi, A., And Hayashizaki, Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
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Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ru, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
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Kagawa, I., Kondo, S., Korno, H., Miyazaki, A., Osato, N., Ota, Y.,
Salto, R., Sasaki, D., Saro, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-nail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 902)
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COMMENT

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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Magata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Mamiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fulimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugano, S., Fulimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Inda, Y., Sugano, S., Fulimura, T., Suzuki, Y., Yekomizo, S., Niikura, J., Kawai, T., Kodama, T., Maruda, H., Koshyashi, M., Xie, O., Lu, M., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Riken, Y., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Komo, H., Miyazaki, R., Ishii, Y., Itoh, M., Hayashizaki, D., Sato, K., Shibata, K., Shinagawa, M., Shiraki, T., Yoshino, M. and Hayashizaki, S., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Solloction, mapping, and annotation of over 28,000 cDNA clones from Collection, mapping, and annotation of over 28,000 cDNA clones from Collection, mapping, and annotation of over 28,000 cDNA clones from Collection, and Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collection, Collecti
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Oryza sativa (japonica cultivar-group) cDNA clone:J023070H02, full
insert sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplande; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 ATTGATAAAGTTAAGATGGAAATAGTGGTGTCCAAGGATCAGGTTGAAGCTGTTGTTGAC
                                                                                                                                                                                                                                                                                                                            CCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCATGGAGAATCCAGCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 TCATCGGGTTTGCTGCAAATGGGGATCAGAGGCGTGACGGTGTCCGACGTGCGGGGGTTTC
                                                                                                                                                                                            Length 902;
                                                                                                                                                                                                                                                       0; Mismatches 106; Indels
                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                           Pred. No. 1.6e-39;
                                                                                                                                                                                                Score 199.4;
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                            33.9%;
al Similarity 71.3%;
263; Conservative
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AUTHORS
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Science 301 (5631), 376-379 (2003)

JOURNAL

/organism="Oryza sativa (japonica cultivar-group)'

Location/Qualifiers

source

PEATURES

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Yamamoco, M.

FAIS Genome Sequencing & Analysis Group: Otoco, Y., Iida, Y.,

FAIS Genome Sequencing & Analysis Group: Otoco, Y., Ikeda, R., Iseda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,

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Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Yoshimura, A., Matuhbara, K. and Murakami, K.

Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninoi, P., Pukuda, S., Hangaki, T.,

Hara, A., Habhizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Itoh, M., Kagawa, I., Kanagawa, S., Karoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Matejawa, T., Miyazaki, A., Murata, M.,

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Sasaki, D., Saro, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Sasaki, D., Saro, K., Shibata, T., Tomaru, A., Toya, T., Waki, K.,

Yasunishi, A., and Hayashizaki, Y.

Iocano, Qualifiers
                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, K., Haysshizaki, Y., Haystsu, N., Hiramoto, K., Hiraoka, T., Horia, I., Iida, J., Ikajetsu, N., Hiramoto, K., Hiraoka, T., Ranagawa, S., Katoh, H., Xawagashira, N., Kawai, J., Kawamara, M., Karaoh, H., Kawagashira, N., Kawai, J., Kawamara, K., Kainimara, K., Kojima, Y., Kojima, Y., Kondo, S., Konno, H., Kodawa, I., Kodawa, S., Kuribara, C., Kurosaki, T., Kishimoto, M., Mouda, M., Kodawa, S., Kuribara, C., Kurosaki, T., Kishimoto, M., Miyazaki, A., Mazubara, C., Kurosaki, T., Kishimoto, M., Myazaki, A., Mazubara, C., Kurosaki, T., Magata, T., Nakamura, M., Nawiki, R., Murakama, K., Mutaka, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Mikura, J., Nishi, K., Oka, M., Ooka, H., Osato, M., Otemo, Y., Sato, M., Satoh, K., Satoh, K., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, T., Shiraki, T., Shishiki, T., Tagama, A., Saro, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Sugamo, S., Shiraki, K., Saicuki, Y., Tagami, M., Tagama, Takeda, T., Tomatu, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomatu, A., Tanakashi, F., Takaku-Akahira, S., Tanaka, T., Tomatu, A., Voshimura, A., Suzuki, K., Sauki, K., Xie, Q., Yahagi, W., Yamamoto, M., Yasumishi, A., Yazaki, J., Yokomizo, Submitted (27-Aug-2002) Shoshi Kikuchi, Mational Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8002, Japan (E-mail:skikuchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Obneda,B., Yahagi,M., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
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Search completed: May 27, 2004, 22:22:44 Job time : 1740.26 secs

organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA" /cultivar="Nipponbare" /db xref="taxon:39947" /clone="J023070H02" 208 CCAGACTCGAAATTTTACAAGGTGGAAGCAATGTCAGACCATGGAGAATCCAGGAAGTT

33.9%; Score 199.4; DB 8; larity 71.3%; Pred. No. 1.6e-39; Conservative 0; Mismatches 106;

Best Local Similarity 263;

Query Match Matches

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DB 8; Length 902; Indels

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 549)
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
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BB311072 EST531282
CA922829 EST640547
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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CAS14765
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Perfect score:
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Total number Minimum DB Maximum DB

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TGCCCAAATAICTTCTGATTATATTCCAGACTCGAAATTTACAAGGTGGAAGCAATTGT 294
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                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
                                                                                                                                                                            266 bp
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="root"
/lab_host="DH10B"
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                                                                                                                                                                                                                       mRNA sequence.
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                                                                                                                                                                                                                                                                                                /CLONE ILLE-WALLE-ALLE | Sall; Site 2: NotI; CDNA library from Arabidopsis thaliana, accession Landsberg erecta; six weeks old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-NotI, primer sites and orientation:
T7-Sall-CCAGGGTCG-Sprime-CDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection PI: Bernd Weisshaar Sequence submission managed by RZDJ/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAGAACAITGCITICTCTGAITGCAITICGAITTGTTCTGGAITCAGACAITCCCGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AAG-ACATTGCTTTCTCTGATTGCATTTCGATTTGTTCTGGATTCAGACATTCTCGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 anggaggggrangacgaaacccarcrcaaraacrrcrcrcggrrrcrarrarrcra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 481; DB 14; Length 549; 97.7%; Pred. No. 1e-124; Live 0; Mismatches 10; Indels 2
                                                                                                                                                                                                  /clone="MpizpT69A094Q"
/tissue type="whole plant"
/dew stage="adult plant"
/lab host="E. coli X11-Blue MRF"
/clone lib="MPIZ-ADIS-012"
                                                                                                                                          erecta (Ler)"
                                                                                                    'organism="Arabidopsis thaliana"
      Plate: 4 row: A column: 09
Seg primer: 17R; CTAATACGACTCACTATAGGGA.
Location/Qualifiers
Std Error: 0.00
                                                                                                                                                             'db_xref="GABI:589834"
                                                                                                                       /mol_type="mRNA"
/cultivar="Landsberg
                                                                                                                                                                                   'db_xref="taxon:3702"
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Matches 509;
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1999).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACATTGCTTTCTCTGATTGCATTTCGATTTGTTCTGGATTCAGACATTCCCGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GAACATTGCTTTCTCTGATTGCATTTCGATTTTCTGCATTCAGACATTCCGGACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trecerceartresicacaaagreaceastaaraacastesistratracersitas 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
449 GAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGATGGAGCAAGGACAGGAGAGT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                           AU236084 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-63-K15 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCGAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids; l. Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                                                     linear
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Plant Punctional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                          549
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/note="Site_1: BamHI; Site_2: SalI"
                                                                          480 TGGTGATGCCAAGATTTTTGTTTTGCCTGTGTCAGATGTCA
                                                                                                                                          509 regrearescaacarrirrerrrreccrerercacardrea
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CD822497
BN25.045G20F020108 BN25 Brassica napus cDNA clone BN25045G20, mRNA
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Mkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 669)
                                                                                                                                                                                                                                                                                        428
  237
                                                                                                        249 AITGTCAGGCCATGGAGAATCCAGCATGTTTCATCGGCTTTACTGAAATTGGGATTCGGA 308
                                                                                                                                                                  298 GGIGTTACTGTTTCTGAIGTGAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACAC 357
                                                                                                                                                                                        417
                                                                                                                                                                                                                                                                                                                            418 AAGAAAGACCAAGTGGAATCTGTAATCCACAATAATTGAAGGAGCAAGGACAGGAAG 477
                                                                                                                                                                                                                                                                                                                                                                     429 AAGAAAGAACAAGTGGAGTCTGTAATCAACACCATAATCGATGGAGGAAGAACAGGAGAAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 Arcedadaroccaaaararrcerrreccrerercaeargrearaaggerregaeagge 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 GTTAGAGCCCAAAGGTCTTATGATTATATTCCAGACTCAAAGTTTTACAAGGGGGGGCA
                                                                                                                                                                                                                                                                         478 ATTGGTGATGGCAAGATTTTGTTTTTGCTGTGTCAGATGTCATAAGAGTTAGGACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGCGCGTCAATGACGAAACCCATCTCCAATAACTTCTCTCGGTTTCTATTCTGATCGA
GITAGTGCCCAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCA
                                                                               238 ATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGA
                                                                                                                                                                                                                                                 358 GGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 GAGCGTGGAGAACAAGCAGAGAAGATGACTGGTGACATGCTTTCGTCATCT 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 GAGCGTGGGGAGAAAGCAGAAGATGACTGGTGATATGCTTTCACCGTCT
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Tel: 33 1 69 47 54 00
Pax: 33 1 69 47 54 10
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85.4%; Pred. No. 9.8e-114;
iive 0; Mismatches 83;
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/mol_type="mRNA"
/cultivar="Jet neuf"
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/clone="BN25045G20"
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/clone lib="BN25"
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BN25.060G17FC11129 BN25 Brassica napus cDNA clone BN25060G17, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 CCATCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae; Brassica.
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                                                                                       362
                                                                                                                                                                                          415 CTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
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                                                                                                                                                                                                                                                                                            475 AGACCAAGTGGGAATCTGTAATCAACACAATAATTGAAGGAGCCANGGACAGGAGAT
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        CAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGTGT
                             TACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGG
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                                                                                                                                                                      CTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAA
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.5%; Score 443.8; DB 14, Sest Local Similarity 85.6%; Pred. No. 3.5e-114; Matches 506; Conservative 0; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                            535 TGGTGATGGCAAGATTTTTGNTTTGCCTGTG 565
                                                                                                                                                                                                                                                                                                                                       TGGTGATGGCAAGATTTTTGTTTTGCCTGTG 510

    . 685
    /organism="Brassica napus"

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/colliva="Jet neuf"
/db_xref="taxon:3708"
/clone="BN25060G17"
/tissue type="seed"
/clone_lib="BN25"
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Brassica napus
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Query Match         75.2%;         Score 442.2;         DB 14;         Length 732;           Best Local Similarity 85.4%;         Pred. No. 1e-113;         Andels 3;         Gaps 1;           Matches 505;         Conservative 0;         Mismatches 83;         Indels 3;         Gaps 1;           1 AndGCGGCTCAATGCAGAACCCATCTCTAATACTTCTCTATTCTATTCTGATCGA 60         AndGCGGCTTCAATGCAACCATCTCTGAAACCTCTCTCGAACCTCTCTCGATTCTCTCTC	118	Qy         238 ATTGTCAGACCATGGAGAATCCAGGAGTTTCATGGCTTTACTGAAAATCGGGATTCGA         297           Db         252 ATTGTCAGGCCATGGAGAATCCAGCATGTTCATCGGCTTTACTGAAAATCGGGATTCGA         311           Qy         298 GGTGTTACTGTTTCTGATGAGAGGTTTGGTGCACAAGGAGGTCTACCGAGAGACAC         357           Db         312 GGTGTGACGGTTTCTGATGTCGAGGGGTTTGGTGCACAAGGTGCACAAGAGAGACAT         371	Qy         358 GGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTT 417           Db         372 GGTGGGTCTGAGTTCTCTGAAGACAAGTTCGTTAAGATGGAGATCGTTGTT 431           Qy         418 AAGAAAGAACAAGTGGAATCTGTAATCAACACAATAATTGAAGGACAAGGACAAGGAGAGAGA	Oy         478 ATTGGTGATGGAGATTTTTGTTTTGCCTGTGTGAGATGTCATAAGAGTTAGGAGGT 537           Db         492 ATGGGAGATGGCAAAATTTTGCTTTTTGCCTGTGTGAGTGCTAAGGGTTCGGAGAGGT 551           Qy         538 GAGCGTGGGAAAGCAGAGAAGATGACTGGTGATATGCTTTCACCGTCT 588           Db         552 GAGCGTGGGGAACAAGAGAGAAAGATGACTGGTGATATGCTTTCACCGTCT 588           Db         552 GAGCGTGGGGAACAAGAAAGAAGAAGATGACTGGTGACTGGTCATCT 602	RESULT 6 CD819046 CD819046 CD819046 CD819046 CD819046 CD819046 CD819046 T45 bp mRNA linear EST 10-JUL-2003 DEFINITION BKZ0.047L06F011226 BNZ0 Brassica napus cDNA clone BNZ0047L06, mRNA ACCESSION CD819046 CD819046.1 GI:32500986 KEYWORDS EST. CD819046.1 GI:32500986 CBYORCE CRANTSW RASSICA napus (rape)	BUKATYOTA Spermatop Spermatop Spermatop Spermatop I Dases Genoplant Contact: Contact: 93, rue 1 Fel: 33 1 Fax: 33 1 This seque plant gen plant gen	FEATURES Location/Qualifiers 1745 fource 1745 /organism="Brassica napus"
SATTCAGACATTCCCGA   117	TGAAAATCGGGATTCGA 297  TGAAAATTGGGATTCGA 301  DD  GTTCTACCGAGAGACAC 357  GATCCAAAGAGACAT 361  DD	417 421 477 481	GGACAGGT 537	NT 10-JUL-2003 8040D05, mRNA	eophyta; s; nomics	re.com	
61 AAGAACATTGCTTTCTCTGATTGCATTTGTTCTGGATTCAGACATTCCCGA  [1]		358 GGTGGCTCTGAGTTCTCGGAACACAAATTTGTTACTAAAGTTAAGATGGAAATCGTTGTT 362 GGTGGCTCTGAGTTCTCTGAAGACACATGCTTACTAAGATTAAGATGGAGATCGTTGTT 418 AAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGAGAGA	478 ATTGGTGATGGCAAGATTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGAC 482 ATCGGAGATGGCAAAATATTCGTTTTGCCTGTGTCAGATGTCATAAGAGTTTGGAC 538 GAGCGTCGGAAAAATATTCGTTTTTGCCTGTTCAGATGACTTCGGAC 538 GAGCGTCGGAGAAAAGAAGATGACTGTTGTTTTTCACCGTCT 588 542 GAGCGTCGAGAAAAAGAAGATGACTGGTGATATGCTTTCGTCATTTCGTCAT 592	0820903 732.040D05F011026 BN25 Brassica napus equence. 0820903.1 GI:32502843	EST.  Brassica napus (rape) Brassica napus Brassica napus Brassica napus Brassica napus Brassica napus Brassica napus Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot rosids; eurosids II; Brassicales; Brassicaceae; Brassica.    (bases   to 732) Genoplante. Genoplante, a major partnership french program in plant ge Unpublished (2003)	Genoplante Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France 93, rue Henri Rochefort 91025 EVRY CEDEX France 1 = 33 1 69 47 54 00 This sequence has been generated in the framework of the plant genomics programme 'Genoplante' (http://www.genoplante.info.infobiogen.fr). 1 = 732 1 = 732   nolltype="mRNA"   molltype="mRNA"   molltype="mRNA"   molltype="mRNA"   cultivar="Jet neuf"   db xref="taxon:3708"   tissue type="seed"   tissue type="seed"	/clone_Tib="BN25"
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V-B-112F06 VAN-Baker-1 Vitis aestivalis CDNA clone V-B-112F06 5',
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Vitis aestivalis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371
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rosids; Vitaceae; Vitis
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                                                                                                                                                                                                                       Length 745;
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Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P.
Expressed sequence tags of young leaf tissues of a disease-resistant Vitis aestivalis var. Norton Unpublished (2003)
Contact: Wemping Qiu
Department of Fruit Science
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                       74.9%; Score 440.6; DB 14;
B5.3%; Pred. No. 2.8e-113;
ive 0; Mismatches 84;
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxor:3708"
/clone="BN20047106"
/tissue_type="seed"
/clone_lib="BN20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB289081.1 GI:28602822
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/dev gtage="Young leaf"
/dev gtage="Young leaf"
/lab_host="Xii0-Gold E .coli"
/lab_host="Young leaf"
/lone lib="YAN-Baker-1"
/note="Vector: pBluescript II SK (+) Phagemid: Site_1: Xho
/site_2: EcoR I; VAN-Baker-1 is a cDNA library of Norton
grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves and library construction was performed
according to the instruction manual for pBluescript II XR
cDNA library construction kit provided by Stratagene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 CITICICIGATIGGATITICGATITICITICIGGATICAGACATICCCGACCATCTTGCCTCG 130
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Southwest Missouri State University-Mountain Grove 9740 Red Spring Road, Mountain Grove, MO 65711-2999, Tel: 417 926 4105
Fax: 417 926 6446
Email: weq070f@smsu.edu
Insert Length: 782 Std Error: 0.00
Plate: VAN-Baker-1-12 row: F column: 06
Seq primer: T3 PRIMER
High quality sequence 8top: 782
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 134; Indels

    .782
    /organism="Vitis aestivalis"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3605"
/clone="V-B-112F06"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Norton"
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Matches 364; Conservative
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Fri

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BE239550 EST 12-JUL-2000
EST403599 MHRP- Medicago truncatula cDNA clone pMHRP-28F3, mRNA
sequence.
                                                                                     AJ558383 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ588383 Antirrhinum majus cDNA clone AJ588383 Antirrhinum majus cDNA clone AJ588383 Antirrhinum majus cDNA clone AJ588383
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                                                                                                                                                                                                                                               Antirrhinum majus (snapdragon)
Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; lamiales; Antirrhinaceae; Antirrhineae;
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472 geláglatregrelnegelalegeletítrirgrectrocagirirorgalalalagagirogo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 252.8; DB 9
Pred. No. 2.9e-60;
0; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Antirrhinum majus"
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MPI fuer Zuechtungsforschung
Carl-von Linne Weg 10, D-50829,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Zachgo, S., Stueber, K., Saec
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
                                                                                                                                                                                                  AJ558383.1 GI:31660955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 43.0%; al Similarity 77.0%; 308; Conservative [
                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 732)
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Best Local S:
Matches 308;
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/clone_lib="Ripening Grape berries Lambda Zap II Library"
/clone_lib="Ripening Grape berries Lambda Zap II, Site_l: Eco
/clote="Organ: Fruit, Vector: Lambda Zap II; Site_l: Eco
/RI; Site_2: XhoI; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"
    BQ798001 723 bp mRNA linear EST 30-JUL-2002 EST 6939 Ripening Grape berries Lambda Zap II Library Vitis vinifera cDNA clone RT093C02 3', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.

1 (bases 1 to 723)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Hambi, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Romieu C.
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0; Mismatches 97; Indels 0;
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Institut National de la Recherche Agronomique
Institut National de 100 Montpellier Cedex 01, France
Tal: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
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/mol type="mRNA"
/cultivar="Shiraz"
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/clone="RT093C02"
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                                                                                                                                               Vitis vinifera
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                               467 GGACAGGAGATTGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAG 526
                                                                                                                                                                                                                              473 GAACTGGGGAGATTGGTGATGGCAAAATTTTCTTGATCCCTGTATCTGATGTAATAAGAA 532
413 AAATAGTGGTGAGAAAAGACCAGGTTGAGGCAGTGATAAACAAAATTATGGAGACGGCAA 472
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Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T.,
Cho, J. and Fraser, C.M.
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/dev_stage="Immature seeds, 11 to 19 days after
pollination"
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More information is available at: www.medicago.org
Seg primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             527 TTAGGACAGGTGAGCGTGGGGAGAAAGCAGAAGATGACTGGTG 571
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1100 Bates Street, Houston, TX 77030-2600, USA
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Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
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/mol type="mRNA"
/cultivar="A17"
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/clone="pgESD9J4"
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Harrison,M.J., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt, L.E., Cho,J. and Fraser,C.M.
ESTs from phosphate-starved roots of Medicago truncatula Unpublished (2000)
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
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More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC)

    .597
    /organism="Medicago truncatula"

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/clone="pMHRP-28F3"
/tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
                                                                                                                                                                                           Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mjharrison@noble.org
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'cultivar="A17"
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613 bp mRNA linear EST 18-MAY-2001
EST281945 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLEC1608, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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extracts. Plasmids containing cDNA inserts were exciss from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AGGIGGAAGCAATIGICAGACCAIGGAGAAICCAGCAAGITICAICGGCITIACIGAAAA
                                                                                                                                                                                                                                                                                                                      Gape
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 1.7e-58;
0; Mismatches 99; Indels
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Generation of BSTs from tomato callus tissue
Unpublished (1999)
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/dev_stage="25-40 days old"
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/cultivar="TA496"
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EST640547 MTUS Medicago truncatula cDNA clone MTUS-58H7, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                       172 ITCTTCCCAAAATCAGGGCTCAAAACCTTCCTGACTATGTTCCTGAATCCAAGTTTTACA 231
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Alias Clone pMERP-28F3
TIGR sequence name: MTUCF91TV
More information is available at: www.medicago.org
Seq primer: (gtA AtA CgA CtC ACT AtA ggg C).
Location/Qualifiers
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/tissue_type="mixed tissues"
/dev_stage="various stages"
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/cultivar="A17"
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                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK(-); Site 1: ECORI; Site 2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 ITCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AGGAGTCATTGCCATGATAATTGAAGAGGCAAGAACTGGTGAAATAGGTGATGGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 ITTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGGCGTGGGGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B1932336 T10wer, 8 mm to preanthesis buds Lycopersicon esculentum cDNA clone cTOC22H10 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GETCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCCAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 GCTCACCTTCAAACGCTGTCAAAATGCTCCTTCTTTCCCGATTATCAGAGCCCAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 recadaritegiecerdargegaagrifiracaaagirgaageaariteraagaeerregag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 245; DB 12; Length 7
Pred. No. 4.6e-58;
0; Mismatches 120; Indels
                                                                                                                                     organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                         /db_xref="taxon:4081"
                         Seq primer: T3.
Location/Qualifiers
1. .702
                                                                                                                                                                                                                                                                                  /clone="cTOC22G23"
                                                                                                                                                                   /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AGAGAGGATGATGGGAG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI932336.1 GI:16246808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.78;
72.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 317; Conserv
Institute
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BI932336
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VERSION
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                             /clone_lib="tomato callus, TAMU"

/clone_lib="tomato callus, TAMU"

/hote="Yector: pRlueScript SK(-): Site_1: EcoR1; Site_2:

/hote="Yector: pRlueScript SK(-): Site_1: EcoR1; Site_2s

/hote="Yector: Glovannoni laboratory; cLEC - Cotyledons

of seedlings 7-10 days post-germination were excised, cut

at both ends and placed on NS medium with no selection.

Mixed callus was harvested at 25 and 40 days and included

undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAATATC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GCTCACCTTCAAACGCTGTCAAAATGCTCCTTCTTTCCCGATTATCAGAGCCCAAAACTC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAGATTTCGTCCCTGATGCGAAGTTTTACAAAGTTGAAGCAATTCTAAGACCTTGGAG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGTGTTACTGTTTCTGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATICAACAGGITTCTTCGGCACTACTGAAATGGGCATTCGTGTCTCACTGTTTCGGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        refregregaritegececcaageregerreacreacaageregecregaarrere 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGAT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGTCATTGCCATGATAATTGAAGAGCAAGAACTGGTGAAATAGGTGATGGAAAGAT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 ATTCTTGACTÓCCATÓTÓCOGÁGTTATAAGAGTTOGCAÓTGGAGAAAGGAGAAAAGGO 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCATGGAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 TTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGCGTGGGGAGAAAGC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, buds 8 mm - preanthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University
100 Oracian Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 TGAAGACACGTTTGTTGCAAAAGTTAAAATGGAAATTGTTGTCAGCAAAGACCAGGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                         Length 613;
                                                                                                                                                                                                                                                                                                                                                     Score 245; DB 9; Length 61
Pred. No. 4.4e-58;
0; Mismatches 120; Indels
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   /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGAAGATGACTGGTG 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:16246595
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                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 72.5
Matches 317; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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EST 18-OCT-2001

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Gaps

6

194 231 254 291 314

351 374 411 434 471 494 531 554

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Seq primer: T3.

Seq primer: T3.

Location/Qualifiers

1.71:
    /organism="Inycopersion esculentum"
    /mol type="mRNA"
    /mol type="mRNA"
    /mol type="T4496"
    /db xref="taxon: 14896"
    /db xref="taxon: 14881"
    /clone="cTGC22H10"
    /tisue=type="flower"
    /flone="taxon: 14881"
    /dev stage="buds 8mm to preanthesis"
    /clone lib="tomato flower, 8 mm to preanthesis buds"
    /note="vector: pBluescript SK(-); Site-1: EcoR1; Site-2:
    /note="vector: pBluescript SK(-); Site-1: EcoR1; Site-2:
    /note Taxon: Cornell University; sequencing: The
    Institute for Genomic Research; Flower buds and flowers
    were taxen from greenhouse plants (4.8 wks old, TA496).
    They were immediately frozen in liquid nitrogen and then
    size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                      Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
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Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, buds 8
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The invention relates to identifying a stress condition to which a plant
                                                     Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
                                                                                         Claim 144; SEQ ID NO 2133; 577pp + Sequence Listing; English
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representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrosse-inducible, and are suitable for genetic engineering of plants
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                                                                                                                          Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening; ss.
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                                                                                        thaliana P-PII CDNA
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                          393 GGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGITAAGATGGAAATTGTTGAG
GGCTCTGAGTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAG
                                                                            421 AAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGACAGGAGTT
                                                                                                              453 AAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATT
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nitrogen assimilation; transgenic plant; herbicide screening; ss.
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                                                                        CAAATATCTTCTGATTATATTCCAGACTCGAAATTTTTACAAGGTGGAAGCAATTGTCAGA
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                                                                                                                                                  GTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCT
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                                                                                                                                                                                                                           GSCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGCTGGG
           CTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Castor bean; PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening;
                                                                                                                                                                                                                                                                                                      GAGAAAGCAGAGAAGATGACTGGTG 571
                                                                                                                                                                                                                                                                                                                 GATAAGGCTGAGAGGATGACAGGAG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                            Ricinus communis P-PII cDNA
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P-PSDB; AAB69496.
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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                          Sequence 897 BP; 254 A; 171 C; 218 G; 254 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 285; DB 4; Length 89
Pred. No. 4.1e-76;
0; Mismatches 165; Indels
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Continuation (2 of 17) of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534
                                                                                                                                                                                                                                                                 The present invention relates to a Moraxella catarhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarhalis (Branhamella catarhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarhalis is known to cause acute, localised infections such as ottics media, sinustics and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
                                                                                                                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 96109 BP; 28783 A; 18910 C; 20341 G; 28075 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 92.8; DB 4; Length 96109; llarity 57.8%; Pred. No. 8.8e-17; Conservative 0; Mismatches 132; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding Acinetobacter baumannii protein #1311.
                                                                                                                                                                                                                                           Claim 1; Page 345-368; 545pp; English
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                                          16-JUN-2000; 2000WC-US016649
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ses 185; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ATTAGTGATGAAATGGTCGACGCGGTAATTGAGTCAATTACACGTGTGGCAAGCACTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 GCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATT
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14.6%; Score 85.8; DB 8;
Best Local Similarity 57.4%; Pred. No. 1.1e-15;
Matches 175; Conservative 0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example, SEQ ID NO 1311; 328pp; English.
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                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
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fragments
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99US-00328352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that anothiate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P.
                                                                                                                                                                                                                                 TGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGATTTT 497
                                                                                                                                                                                                                                                                                                                          Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
TTATAAAAATGAGGTTGAGATTATGAAAAAGTTGAAGCAATCATAAGACGGAGAAGTT
                                                                             13344 GGAGATTGTTAAAAAGGCTTTGTCTGATGCTGGGTATGTTGGAATGACTGTTAGTGAGT
                                                                                                             GAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTCGGA
                                                                                                                                          13284 TAAGGGTAGGGCAGTTCAAGGTGGAATAGTTGAGAGGTATAGGGGGGAGAGAGTATATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                 CCAGCAAGTTTCATCGGCTTTTACTGAAAATCGGGATTCGAGGTGTTACTGTTTCTGATGT
                                                                                                                                                                      AGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAAGACCAAGTGGAATC
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Buchrieser
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LOCUS AAV21209 Accession Aav21209
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                                                                                                                                                                                                                                                                                                                                                                                                                                        337 GGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAA
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Pred. No. 2.9
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                                                                                                                                                                                                                                                                                  181; Conservative
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Continuation (15 of 17) on the Sequence split into 17 WP Sequence split into 17 WP AAV21209_01
WP AAV21209_02
WP AAV21209_03
WP AAV21209_04
WP AAV21209_06
WP AAV21209_06
WP AAV21209_06
WP AAV21209_08
WP AAV21209_08
WP AAV21209_11
WP AAV21209_11
WP AAV21209_12
WP AAV21209_13
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AAV21209_03
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AAV21209 12
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AAV21209 16
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198 IGAITATATICCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCCATGGAGAAT 257

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(Photorhabdus luminescens nucleotide Accession Acf65387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49427 ATACAGAGCTGTATCGCGGTGCAGATATATGGTGGAT---TTTCTGCCAAAAGTGAAAA 49483
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Pred. No. 2.8e-13;
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s LOCUS ACF65387
End
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WP Sequence split into 7

WP ACFGSS97

WP ACFGSS97

WP ACFGSS97

WP ACFGSS97

WP ACFGSS97

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WP ACFGSS97

WP ACFGSS97
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ACE67367 39
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ACE67367 31
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ACE67367 33
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ACF67367_27
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ACF67367_29
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ACE67367_43
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ACF67367_45
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ACF67367_41
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ACF67367_52
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LOCUS ACF67367 Accession Acf67367
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                recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The egenes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 ACAAGGIGGAAGCAAIIGICAGACCAIGGAGAAICCAGCAAGIIICAICGGCIIIACIGA
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                                                                                                                                                                                                                                                                                         Gaps
    luminescens. Cells transformed to express the genes are useful for
                                                                                                                                                                                                                                                 13.8%; Score 81.4; DB 7; Length 339; 55.0%; Pred. No. 2.3e-14; tive 0; Mismatches 146; Indels
                                                                                                                                                                                                               Sequence 339 BP; 105 A; 51 C; 96 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTTAGGACAGGTGAGCGTGGGGAGAAGC 554
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WP Sequence split into 57 fragments
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Best Local Similarity 55.0
Matches 182; Conservative
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ACF67367 03
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ACF67367_11
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ACE67367_18
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ACE67367_21
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64096 TGGAAGTGGTAGTTCCTGATGAGCTTGTGGATCAATGTATTGAAGCGATTATTGAAACGG 64155
                                                                             64156 CACAAACAGGIAAAAICGGIGACGGAAAAITITITITITATCACGIITGAGAGAGCCAICC 64215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 ATACGGAAATCTATCGCGGTGCGGAATACGCCGTCGAT---TTCCTGCCCAAGGTCAAAA 208
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                                      464 CAAGGACAGGAGAGATTGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and comparisons that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 adaticisciatitacesiscatisacisticas estas estas adas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas estas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 77; DB 7; Length 363; Pred. No. 5.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; infection; vaccine; gene therapy; gene; ds.
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                                                                                                                                                                      64216 dearregeaceaceaaaaaaaceaaree 64246
                                                                                                                                                                                                                                                                                                                                                                                                                  gonorrhoeae nucleotide sequence SEQ ID 4633
                                                                                                                               524 GAGTTAGGACAGGTGAGCGTGGGGAGAAGC 554
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                                                                                                                                                                                                                                                                                     ВР
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54.1%;
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                                                                                                                                                                                                                                                                                     DNA; 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae
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Matches
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19 fragments LOCUS AAT42063 Accession AAT42063
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                                                                                                                                                        88821 AAAAGATTGATGCGATTATGAAGCTTTCAAATTAGATGATGTGCGTGAAGCTCTGGCGG 88880
                                                                                                                                                                                                                                            88881 AAGTGGGTATCACCGGAATGACAGTAACAGGTGAAAGGTTTTGGGCGCCAAAAAGGTC 88940
                                                                                                                                                                                                                                                                                                                                   88941 ATACAGAGCTSTATCGCGGTGCAGAATATATGGTGGAT---TTTCTGCCAAAAGTGAAAA 88997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89058 CACAGACCGGGAAAATCGGTGATGGTAAAATATTTGTATTTGATGTAGCACGTGTTGTGC 89117
                                                                      Η;
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Pred. No. 8.4e-13;
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that may be presumed targets for the immune system and which are rantigenically variable or at least more conserved than other more

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                         CAAGGACAGGAGAGATTGGTGATGGCAAGATTTTTTGTTTTGCCTGTGTCAGATGTCATAA 523
                                        269 cecerregecaaaareesceacescaacarrrrrerecrecesreagearecaarec 328
                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                   N. meningitidis partial DNA sequence gnm_20 SEQ ID NO:20
                                                          524 GAGTTAGGACAGGTGAGCGTGGGGAGAAAGCAG 556
                                                                     329 GTATCCGCACGGGGGAACGTTCGGACGCGGGG 361
                                                                                                                   AAA81472 standard; DNA; 16526 BP
                                                                                                                                                                                                                                                                    99WO-US023573.
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent pecifically claimed Neisseria meningidia genomic DNA sequences. AAA81260 to AAA81203 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81240 to AAA81221 represent PCR primers used in the isolation of AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis MenB polyrucheotide ORF sequences, which are all used in the exemplification of the present invention. The mucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition of the present invention. The used is medicament (or in the manufacture of a medicament) for treating, the manufacture of a medicament) for treating, corresponding or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all apply pathogenia Neisserial abeterium and all and apply and antibodies and and application of sequences from the bacterium and all and apply and antibodies and and apply and antibodies and and apply and antibodies and and apply and antibodies and and apply and antibodies and and apply and antibodies and and apply and antibodies and anti

will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also ben tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins

Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.

Claim 7; Page 466-471; 1760pp; English.

Scarlato V;

Tettelin H, Venter JC; Ratti G, Scarselli M,

Peterson J, C, Mora M,

Frazer CM, hit daleott.

(CHIR ) CHIRON CORP.

WPI; 2000-318079/27.

Hickey E, Galeotti

98US-0103794P. 99US-0132068P.

09-0CT-1998; 30-APR-1999;

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                                                                                      Sequence 16526 BP; 3183 A; 4006 C; 5067 G; 4268 T; 0 U; 2 Other;
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                                                                                                                                       Length 16526;
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12.4%; Score 73; DB 3; Length 165
Best Local Similarity 55.3%; Pred. No. 4.4e-11;
Matches 184; Conservative 0; Mismatches 145; Indeis
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GenCore version 5.1.6
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[ (bases 1 to 594)

Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 617275-A 16 23-JAN-2001;
Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL FEATURES

Unknown. Unclassified. Unknown.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	R1255592 R1255592 R1255592 R1255592 R1255592 R1255592 R1255593 R1255593 R1255593 R1255589 R1255589 R1255589 R125589 R125589 R125589 R12599 R12	linear PAT 16-MAY-2001
SUMMARIES	AR125592 AR125592 AR125592 AR125591 AR125591 AR125591 AR125599 AR125599 AR125599 AR125599 AR125599 AR225199 AR225199 AR225199 AR221185 AY441185 AY441185 AY441185 AY441185 AY641185 AY641185 AY641185 AY641185 AY641185 AY641185 AY641185 AY641185 AY641185 AR271569	ALIGNMENTS 594 bp DNA ent US 6177275.
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/mol_type="mRNA"
/db_xref="taxon:3988"
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Ricinus communis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I: Malpighiales; Euphorbiaceae; Acalyphoideae;
Acalypheae; Ricinus.
1 (bases I to 040,
Hsieh, M.H., Lam.H.M., van de Loo, F.J. and Coruzzi, G.
A PII.like protein in Arabidopsis; putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York University, 100, NY 10003, USA
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M., Direct Submission
Submitted (22-SEP-1998) Biology, New York University, Hashington Square East, New York, NY 10003, USA
Location/Qualifiers
AF095454 840 bp mRNA, linear Ricinus communis PII protein mRNA, partial cds. AF095454
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                                2 (bases 1 to 796)
Garcia-Ibilcieta,D. and Sengupta-Gopalan,C.
Direct Submission
Submitted (22-FEB-2001) Molecular Biology Program, New Mexico University, Corner of Knox and College, Las Cruces, NM 88003, Incestion/Qualifiers
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llarity 72.0%; Pred. No. 2.8e-72;
Conservative 0; Mismatches 153;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 591)
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              Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 2133 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations (CR)
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
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Pred. No. 4.5e-68
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/organism="Arabidopsis tha
/mol type="unassigned DNA"
/db_xref="taxon:3702"
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Best Local Similarity 70.3%;
Matches 397; Conservative
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                      1 (bases 1 to 588)
Coruzzi, G.M., Lam, H.-M. and Hsieh, M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 15 23-JAN-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                     /organism="unknown"
/wol_type="unassigned DNA"
      US 6177275
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      Sequence 15 from patent AR125591 GI:14111653
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67 ATTGCTTTCTCTGALTGCALTTCGALTTCTGGALTCAGACALTCCCGACCALCTTGC 126
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                                                 TTTAACACCGCGGTCAAGCGCGTAAGATATGCC----CCCGTCGTTCCTGTGATTAATGCC
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Pred. No. 4.7e-68;
0; Mismatches 165; Indels
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H,
Platt nitrogen regulatory P-PII genes
Patent: US 6177275-A 13 23-JAN-2001;
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AR125589
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LVTKSPSNNSRVLPVVSAQISSDYIPDSKFYKVBAIVRPWRIQQVSSALLKIGIRGVT
VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMEIVVKKDQVBSVINTIIRGARIGEI
Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Carninci,P.,
Chan,M. M., Chang,C.H., Dale,J.W., Hayashitashi,Y., Hauan,V.W.,
Ishida,J., Jones,T., Kanina,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Sarou,M., Seki,M.,
Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K.,
Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and
                                                                                                                                                                                                                                   Unpublished

Z (bases 1 to 591)

Kim,C.J., Ghen,H., Cheuk,R., Shinn,P., Bowser,L., Carninci,P.,

Kim,C.J., Ghen,H., Cheuk,R., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Southwick,A., Tang,C.C., Torunmi,M., Sakurai,T., Saku,M., Seki,M.,

Southwick,A., Tang,C.C., Torunmi,M., Wong,C., Wu,H.C., Yamada,K.,

Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and
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Submitted (14-MRZ-2003) Salk Institute Genomic Analysis Laboratory
(SIGMAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Bcker, J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN arbidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL DDAS: Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Chee,J.M., Lin,J., Miranda,M., Nguyen,M., Onoders, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yunan,S., Davis,R.W., Theologis,A., and
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    /note="P II nitrogen sensing protein GLB I"

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Pred. No. 4.5e-68;
0; Mismatches 165; Indels
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/note="This clone is in pUNI 51"
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/protein_id="AA063273.1"
/db_xref="G1:28950699"
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/clone="U23463"
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AY442185 947 bp mRNA linear PLN 15-NOV-2003
Lycopersicon esculentum PII-like protein (GLB1) mRNA, complete cds.
AY442185
                                                                                                                                  67 ITCCCTGTTTTGATTTCAGTTTGTTCAGAGCTTAGACATTCTCGGTTTTCTCAC 126
                                                                                                                                                                       97 AİTGÖİLTİÇİĞİİLGAİTİTĞATİTĞITÜLĞBATİCAĞAĞATİÇÜĞACCATÖTTĞÜ 156
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                         37 ecercaangaceaaacecancicaanaacircicicegrirciaircigaregaaagaac 96
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Walch-Liu, P., Roemheld, V. and von Wiren, N.
Direct Submission
Submitted (17-OCT-2003) Institute of Plant Nutrition, Hohenheim University, Fruwirthstr. 20, Stuttgart 70593, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                CAAAGCTCGCCTGACTTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGG
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                                                                                                                                                                                                                          127 TTTAACACCGCGCTCAAGCGCGTAAGATATGCC---CCCGTCGTTCCTGTGATTAATGCC
  <u>ب</u>
Mismatches 165; Indels
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Walch-Liu, P., Roemheld, V. and von Wiren, N.
A PII-like protein in tomato
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/db_xref="taxon:4081"
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/note="LeGLB1"
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LUTKSPSNNSRVLPVVSAGISSDYIPDSKFYXYRAIVRARQVSSALLKIGTRGVT
VSDVRGFGANGGCSTERHGGSEFSEDKFVAKVMELIVKKDQVESVINTIIBGARTGEI
GDGKIFVLPVSDVIKVRTGERGEKAEKAEKATGDHLSPS"
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                                                                                             279 CCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTTCGAGGTGTTACT 338
                                                                                                                                         GITTCTGATGTTCGAGGTTTTGGTGCTCAAGGTGGTTCAACTGAGAGGCAGGGCGGCTCA 363
                                                                                                                                                                                                                               423
                                                                                                                                                                                                                                                                         399 GAGTICTCGGAAGACAAATTIGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAAAGA 458
                                                                                                                                                                                                                                                                                                                     CAGGITGAGGATGITATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGTTGGAGAC 483
                                                                                                                                                                                                                                                                                                                                                                 518
                                                                                                                                                                                                                                                                                                                                                                                                           543
                                                                                                                                                                                                                                                                                                                                                                                                                                                       578
                                                                                                                                                                                   339 GTTTCTGATGTGAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCT 398
    CAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGA 278
                                                CCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACT 303
                                                                                                                                                                                                                               GAATTITCIGAAGACAAGITIGITGCIAAAGITAAGAIGGAGAICGIGGITAGCAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                           484 GGCAAGATTTTCTTGCTGCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         519 GGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGGG
                                                                                                                                                                                                                                                                                                                                                               459 CAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGAT
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Submitted (29-SEP-189) Biology, New York University, 100 Washington Square East, New York, NY 10003, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13965-13970 (1998)
99030678
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/note="GLB1"
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="IV"
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Pred. No. 4.7e-68;
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Arabidopsis thaliana
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/protein id="AAC78333.1"
/db_xref="GI:3885943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 GATAAGGCTGAGAGGATGACAGGAG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 GAGAÁAGCAGAGAAGATGACTGGTG 603
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70.3%;
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TITLE
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SOURCE
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RESULT

CDS

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2. [Dabes 1 to 902]
B. Adachi, J., Alizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hiraoka, T., Horta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Hori, F., Hotta, I., Iida, J., Itda, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katch, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Katch, H., Kawagashira, N., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodas, H., Matsubara, C., Murosaki, T., Musmegi, T., Ii, C., Lu, M., Masuda, H., Matsubara, C., Musoyama, T., Musma, T., Myazaki, R., Matsubara, C., Musoyama, T., Mushi, K., Murakami, R., Muraka, M., Nohata, T., Makamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Oka, M., Ooka, H., Osato, N., Cano, M., Ottsuki, K., Caka, M., Coka, M., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Sugano, S., Sugawa, A., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoka, M., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Proper Shanaga, M., Waki, K., Xie, Q., Yahagi, W., Panana, S., Manada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Proper Shanaga, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Proper Shanaga, M., Yasunishi, A., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J., Yazaki, J.,
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                                                                                                                                                      Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                  Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@mias.effrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
Yoshimura, A., Miura, J.,
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                                                                                                                                                                                                                                                                                                                                                                          Science 301 (5631), 376-379 (2003)
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VRGFGAQGGLTBRQAGSBFSEDTFVAKVMEIVVSKDQVEGVJAKIIBERARTGEIGGG
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AGATTTCGTCCCTGATGCGAAGTTTTACAAAGTTGAAGCAATTCTAAGACCTTGGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TCAACAGGTTTCTTCGGCACTACTGAAATGGGCATTCGTGGTGTCACTGTTTCGGATGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AGACACGITIGITGCAAAAGITAAAATGGAAATTGTTGTCAGGAAAGACCAGGTTGAAGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 TGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGATTGGAGACGGCAAGATTTT 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AGICATIGCCAAGATAATIGAAGAGGCAAGAACTIGGTGAAATAGGTGATGGAAAGATAFIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGGTCAAGCGCGTAAGATATGCCCCCGTCGTTCCTGTGATTAATGCCCCAAAGCTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 CTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTCTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                               note="similar to nitrogen regulatory protein PII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.3%; Score 275.2; DB 8; Length Best Local Similarity 75.9%; Pred. No. 2.5e-65; Matches 340; Conservative 0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                          <IFLTPISDVIRVRTGERGEKAERMMGGHADMSSALSTS'</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555 GAGGATGACAGGAGGCGATCTGACATG 582
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Rujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashizada, K., Hayashizaki, Y., Hayatsu, M., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imamura, K., Imahishi, J., Ishii, Y., Ishikawa, M., Itoh, W., Kagawa, I., Kanagashira, N., Kawai, O., Kawamata, M., Kikuchi, S., Kishikawa Hirozaha, T., Kushimoto, M., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodas, S., Kurnbara, C., Mursaki, T., Musumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Namura, M., Sarai, K., Oka, W., Ota, W., Ota, W., Ota, W., Ota, W., Ota, W., Ota, W., Ota, W., Sano, H., Sasaki, D., Sato, K., Satoh, K., Salibata, K., Sugamo, S., Sasaki, D., Sato, M., Sugamo, S., Takaku, M., Tagami, M., Tagami, Takama, A., Takahashi, F., Takaku, A., Tagami, M., Tagami, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, R., Yazaki, J., Yokomizo, S. and Yoshima, M., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshima, S., Lanta, A., Yanagi, W., Satoh, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., Sana, S., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahasti, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
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/cultivar="Nipponbare"
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Matches
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JOURNAL
REPERENCE
                                                    AUTHORS
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Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ouneda,E., Yahagi,W., Suzuki,X., Li,C.,
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Kurosaki,T., Kodama,T., Maxuda,H., Kodayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Kusumegi,T., Oka,M., Kawamata,M., Yokimizo,B., Miura,J.,
Kusumegi,T., Oka,M., Ryatau,M., Yadimura,R., Miura,J.,
Kusumegi,T., Oka,M., Hayatau,N., Imcamik,, Arakawa,T., Fukuda,S.,
Hara,A., Hashindume,W., Hayatau,N., Imcamik, . Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Saaski,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
Japonica rice
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FLI CONA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enhartoideae, Oryzeae, Oryza.
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0; Mismatches 118;
                                                                                                                                                                                                   36.4%; Score 216.2;
llarity 70.9%; Pred. No. 6.1%
Conservative 0; Mismatches
          /db_xref="taxon:39947"
/clone="J013149B08"
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es 287; Conserv
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Pinus; Pinus.
GCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTC
                           327 GAGGGTGCCTTATGTGTCATCGGTTTGCTGCAAATGGGGATCAGAGGCGTGACGGTGTCT
                                                             TGATGTTCGAGGTTTTGGTGCTCAAGGTGGTTCAACTGAGAGGCAGGGCGGCTCAGAATT
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Spermatophyta, Coniferopsida, Coniferales, Pinaceae,
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Pinus pinaster mRNA for PII-like protein (glb gene)
AJ489604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="PII-like protein"
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'db xref="GI;37653227"

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/organism="Pinus pinaster"
/mol_type="mRNA"

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/dev_stage="adult_tree"
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glb gene, PII-like protein.
Pinus pinaster
Pinus pinaster
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CCTGACTACATICCTGAIGCIAAATICTACAAAGIGGAAGCAATICICAGGCCCIGGCGA 252
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                                                                                                                              387 ATCTCCCATGTGACTACGGGTCTATTGAAAATGGGGATTCGTGGCGTAACTGTCTCTGAT
                                                                                               GICTOSCAASTITICCTOGGCTITIGCTAAAATIGGTATICGAGGTGTTACTGTTICTGAT
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USA
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
1 (bases 1 to 686)
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Nostoc punctiforme PII (glnB) gene, complete cds.
AF017419
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Hanson, T.E. and Meeks, J.C.
Direct Submission
Submitted Octoward-1997) Section of Microbiology,
California, One Shields Avenue, Davis, CA 95616,
Location/Qualifiers
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/strain="ATCC29133; PCC 73102"
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/db_xref="taxon:63737"
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/gene="glnB"
/function="putative
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/db_xref="GOA:091422"
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RYRGSEYTVEFLQKIKVEIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRI
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Submitted (14-DEC-1999) Zhang C.C., Laboratoire de Chimie
Bacterienne, C.N.R.S., 31, chemin Joseph Aiguier, 13402 Marseille
cedex 20, FRANCE
Location/Qualifiers
                                                                      214 AAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCT
                                                                                                                                               274 ITGCTAAAATIGGTAITCGAGGIGITACIGITTCIGAIGTTCGAGGTTTTGGTGCTCAA
                                                                                                                                                                                                                     334 GGTGGTTCAACTCAGGGCAGGCCGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAA
                                    Gaps
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                    3,
Length 686;
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PII protein.
 Score 107; DB 1; Length 68
Pred. No. 1.3e-18;
0; Mismatches 125; Indels
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Mostoc sp. PCC 7120 (Anabaena sp. PCC 7120)
Nostoc sp. PCC 7120
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codon start=1
trans1_table=11
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Anabaena sp. PCC7120 glnB gene for
AJ251822
AJ251822.1 GI:6983586
GlnB gene: p77
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/protein_id="CAB75358.1"
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/organism="Nostoc sp. PC
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  DB 1;
                                            0; Mismatches 138;
Score 103.2; DB 1
Pred. No. 1.7e-17;
Query Match 17.4%;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

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Database :

The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants Novel P-PII genes capable of requiating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters. Castor bean; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; ss. Ricinus communis P-PII cDNA fragment. Claim 2; Col 37-38; 35pp; English. 97US-00899330. Hsieh M AAF58584 standard; cDNA; 594 96US-0022328P (UNNY ) UNIV NEW YORK STATE. Coruzzi GM, Lam H, WPI; 2001-158572/16 Ricinus communis. P-PSDB; AAB69496. US6177275-B1 23-JUL-1997; 24-JUL-1996; 23-APR-2001 23-JAN-2001. AAF58584; RESULT 1 AAF58584 

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match Length

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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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nitrogen assimilation; transgenic plant; herbicide screening;
                                   4; Length 594;
Sequence 594 BP; 149 A; 117 C; 157 G; 171 T; 0 U; 0 Other;
                                                                      0; Indels
                                   100.0%; Score 594; DB 4; L
100.0%; Pred. No. 2.1e-168;
iive 0; Mismatches 0;
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                                                     larity 100.0%;
Conservative (
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                                 Query Match
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Matches 594; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitros screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ATTGCTTTCTCTGATTGCATTTCGATTTGTTCTGGATTCAGACATTCCGGACCATCTTGC 126
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                                                Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII;
nitrogen assimilation; transgenic plant; herbicide screening; ss.
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al Similarity 70.3%; Pred. No. 2.5e-75;
397; Conservative 0; Mismatches 165; Indels
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                      Arabidopsis thaliana P-PII cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                           Claim 2; Col 37-38; 35pp; English
                                                                                                                                                                                                                                           Hsieh V;
                                                                                                                                                                 97US-00899330.
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{first entry}
                                                                                     Arabidopsis thaliana
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                                                                                                                                                               23-JUL-1997;
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23-APR-2001
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ceil has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome: and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
424 CAGGTTGAGGATGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGTTGGAGAC 483
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                                                    GGCAAGAITTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGGT
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48.0%; Score 285; DB 6; Length 591;
Best Local Similarity 70.3%; Pred. No. 2.5e-75;
Matches 397; Conservative 0; Mismatches 165; Indels
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                  GITICIGAIGIICGAGGITITIGGIGCICAAGGIGGIICAACIGAGAGGAAGGCAGGCGCCICA 363
                                                                                                     CAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGA
                                                                                                                                                                                                                        TICCCIGITITIGATITICAGITITIGICCAGAGCITAGACATICTCGGTITICTCAC
               TITAACACGCGGGGCGTAAGAIAIGCC----CCCGTCGIICCIGIGAIIAAIGCC
                                                             127 crcearriggicacaaagrcacceagraaraacagrcgrgiriracrgrgrgrgrgcc
                                                                                 CAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGG
                                                                                                                          CCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAAATTGGTATTCGAGGTGTTACT
                                                                                                                                              247 ccarggagarccagcaagrircarcggcriracrgaaarcgggarrcgaggriracr
                                                                                                                                                                                      307 GITICIGAIGIGAGGGTITIGGTGCACAAGGAGGTICIACCGAGAGACACGGTGGCTCT
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from base 100001 (Methanococcus jannaschii circular of LOCUS AAV21209 Accession Aav21209
                                                                                                                                                                                                                                                              1;
The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light—and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                                                                                                                                                                                                       Score 285; DB 4; Length 817;
Pred. No. 2.9e-75;
0; Mismatches 165; Indels
                                                                                                                                                                                      Sequence 817 BP; 242 A; 137 C; 188 G; 250 T; 0 U; 0 Other;
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                                                                                                                                                                                                                           Query Match 48.0%;
Best Local Similarity 70.3%;
Matches 397; Conservative (
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AAV21209 01

Continuation (2 of 17) of WP Sequence split into 17

WP Fragment Name WP AAV21209 01

WP AAV21209 02

WP AAV21209 04

WP AAV21209 05

WP AAV21209 06

WP AAV21209 06

WP AAV21209 06

WP AAV21209 06

WP AAV21209 06

WP AAV21209 06

WP AAV21209 07

WP AAV21209 07

WP AAV21209 08

WP AAV21209 08
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13224 TG---ATTTAATTCCAAAGGTTAAGATTGAGTTGGTTGTAAAAGAGGAAGATGTTGATAA 13168
                                                                                                                      12953 GCAATTATCAAGCCGTTTAAACTCGATGATGTGCGAGAAGCACTCTCAGAAATTGGCGTC 13012
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bronchopulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28549. The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as ottics media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                              13107 CGTCATACCAGTAGAAAGAGTCGTAAGAGTAAGAACAAAAGAAGAAGAAAGGAAAAGGGG 13051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                               375 AGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAAGACCAGGTTGAGGA
                                                                                                435 TGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGATTGGAGACGGCAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 GCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATT
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                                                                                                                                                                    CITGCTGCCTGTTTCAGATGTAATAAGAGTCCCCACTGGTGAGCGGGGTGATAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 96109;
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Pred. No. 4.9e-14;
0; Mismatches 137; Indels
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Best Local Similarity 56.24;
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patterson
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LOCUS AAV21209 Accession Aav21209
                                                                                                                                                                                                                                                                                                                                                                                                                            81068 GTTAAGATTGAATTGGTTGTAAAAGAGGAAGATGTTGATAATGTTATTGATATATATATGC 81127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13404 TIATAAAATGAGGITGAGATTATGAAAAAGITGAAGCCAATCATAAGACCGGAGAAGIT 13345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGAGGCAAGAACTGGAGAGATTGGAGACGCCAAGATTTTCTTGCTGCCTGTTTCAGAT
                                                                                                                                                                                                                        AAAATGAAAAAAGTTGAAGCAATCATAAGACCGGAGAAGTTGGAGAATTGTTAAAAAGGCT
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                                                                                                                                                                                     214 AAATICTACAAAGIGGAAGCAATICTCAGGCCCTGGCGAGTCTCGCAAGTITCCTCGGCT
                                                                                                                                                    3; Gaps
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                                                                                                                  DB 2; Length 110000;
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                                                                                                                  Score 96.4; DB 2; I
Pred. No. 1.7e-17;
0; MiBmatches 136;
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Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81188 Grceraagageraagaacaaagagger 81217
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AAV21209 14/c
Cantinuation (15 of 17) of AAV21209
WP Sequence split into 17 fragments
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56.3%;
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57.9%;
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                                                                                                                                      al Similarity 57.9
191; Conservative
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AAV21209_06
AAV21209_07
                                               AAV21209 14
AAV21209 15
AAV21209 16
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AAV21209_09
AAV21209_10
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AAV21209_16
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AAV21209_13
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AAV21209_03
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AAV21209_05
   AAV21209 11
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                                                                                                                       Query Match
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13190 AAAATTGGTGATGGTAAGATTTTTGTTAGTCGCTTGAGCGTGTCATTCGCATTCGAACT 13249
13013 AATGGTATCACCGTCACTGAAGTCAAAGGCTTTGGTCGCCAAAAAGGTCATACCGAGATG 13072
                                                                      13073 TATCGTGGGGCGGAATATGTGGTTGAT---TTTTTACCAAAAATTAAAATTGAGATAGCA 13129
                                                                                                                                          13130 TGTCGTGATGAGATGGTTGAATTATTGAGTCAATCATTAAAGTTGCAAATACAGT 13189
                                                                                                                                                                                 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                    411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for disgnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                  352 CAGGGCGCCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTG
                                                                                                        412 GTTAGCAAAGACCAGGTTGAGGATGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGA
                                                                                                                                                                                 472 GAGATTGGAGACGCCAAGATTTTCTTGCTGCTGTTTCAGATGTAATAAGAGTCCGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Acinetobacter baumannii protein #1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example, SEQ ID NO 1311, 328pp; English.
                                                                                                                                                                                                                                                                                           GGCGAATTTGATGAAAGTGC 13269
                                                                                                                                                                                                                                                           GGTGAGCGGGGTGATAAGGC 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; plant biocontrol agent
                                                                                                                                                                                                                                                                                                                                                                                      ADA30024 standard; DNA; 375 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00328352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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P-PSDB; ADA34150.
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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that andulate, radulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P.
                                                                                      112 Caagggafraccsfaachgaagfraaaggfriffgsfcsfcacaaagacaracagaactr 171
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                                                                                                                                                                                                                                                                                                          289 aaaatedeceaceeraadattititefeactaatetesaacaackafeatecetatedetaca 348
Antibacterial, fungicide, insecticide, polymorphism, genetic analysis, detection, food; gene expression; plant, animal; microorganism, toxin, antibiotic; biopesticide; virulence factor; disease model, plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                   CGAGGTGTTACTGTTTCTGATGTTCGAGGTTTTTGGTGCTCAAGGTGGTTCAACTGAGAGG
                                                                                                                            CAGGGCGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTG
                                                                                                                                                              172 raccecesecreagrareregricar -- rrcrraccraaagraaaareeaaarreee
                                                                                                                                                                                                                                       229 ATTAGTGATGAAATGGTCGACGCGGTAATTGAGTCAATTACACGTGTGGCAAGCACTGGA
                                                                                                                                                                                                                                                                           472 GAGATTGGAGACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photorhabdus luminescens nucleotide sequence #10494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 10494; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                    532 GGTGAGCGGGTGATAAGGCTG 553
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Buchrieser
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14.1%; Score 83.6; DB 8; Length 3 Similarity 55.9%; Pred. No. 9.5e-15; 00; Conservative 0; Mismatches 139; 'Indels

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om base 300001 (Photorhabdus luminescens nucleotide LOCUS ACF65387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49307 AAAAGATTGATGCGATTATCAAACCTTTCAAATTAGATGATGTGCGTGAAGCTCTGGCGG 49386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49367 AAGTGGGTATCACCGGAATGACAGTAACAGAGGTGAAAGGTTTTGGGCGCCAAAAAGGTC 49426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49427 ATACAGAGCTGTATCGCGGTGCAGAATATATGGTGGAT---TTTCTGCCAAAAGTGAAAA 49483
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Pred. No. 5.5e-13;
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ACF65387_6
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ACF67367 52
Continuation (53 of 57) of ACF67367 from base 5200001 (Photorhabdus luminescens nucleoting Sequence split into 57 fragments LOCUS ACF67367 Accession Acf67367
WP ACF67367 00 110000
WP ACF67367 01 100001 210000
WP ACF67367 03 30001 410000
WP ACF67367 04 400001 310000
WP ACF67367 04 400001 510000
WP ACF67367 05 600001 710000
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luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
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                                                                                                                                                                                                                                       Seguence 339 BP; 105 A; 51 C; 96 G; 87 T; 0 U; 0 Other;
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                                   461 CAAGAACTGGAGAGATTGGAGACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAA 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 7; Length 363;
Pred. No. 9.1e-13;
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                                                                                                                                                                                                                                                                                                                                                             Antibacterial; infection; vaccine; gene therapy; gene;
                                                                                                                                                                                                                                                                                                                           N. gonorrhoeae nucleotide sequence SEQ ID 4633.
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                                                                                                                                      64216 GCATTCGCACGGCGA 64231
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                                                                                                      521 GAGTCCGCACTGGTGA
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Matches 180; Conservative
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P-PSDB; ABP79052.
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                   Score 81.4; DB 7; Length 1
Pred. No. 5.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCCGCACCGGTGAGCAGGATGAAGAGGC 89148
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Sequence split into 19 fragments
                   13.7%;
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AAT42063 13

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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81260 to AAA82601 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA812121 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA8122 to AAA8159 and Neisseria meningitidis DNA sequences; and AAA8122 to AAA81452 represent Neisseria meningitidis MenB polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For
209 TCGAGTTGGTGGTGGATGCCGTGGAACGCGCGATTGACGTGATTGTCGAGGTGG 268
                                                                                                        269 CGCGTTCGGGCAAAATCGGCGACGGCAAGATTTTTGTGCTGCCGGTCGAGGAGGCAATCC 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against Meningococcus B; against all serctypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin H, Venter JC;
Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                              CAAGAACTGGAGAGATTGGAGACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleotide sequences of Neisseria meningitidis which can be un the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                    N. meningitidis partial DNA sequence gnm_20 SEQ ID NO:20.
                                                                                                                                               521 GAGTCCGCACTGGTGAGCGGGTGATAAGGCTG 553
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30-APR-1999;
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that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more
                                                                                                 Sequence 16526 BP; 3183 A; 4006 C; 5067 G; 4268 T; 0 U; 2 Other;
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                                                                                                                                              Query Match 12.3%; Score 73; DB 3; Length 16526; Best Local Similarity 55.3%; Pred. No. 8e-11; Matches 184; Conservative 0; Mismatches 145; Indels 4
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CF920467 gmrhRww3-BI932336 BST55225 AJ558383 AJ558383 AI773079 EST254179

EST552802 EST339498

AW738071

BI932123 EST552012 BI932913 EST552802

AW035791 EST281945

CA922829 EST640547 BF645522 NF036F08E

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T15252 542 bp mRNA linear EST 23-MAY-2001 cr8852 lambdaZAPST Ricinus communis cDNA clone pcr8852 similar to
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1 (Dases I to 542)
vandeloo,F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CR 94305
                                                                                                                                                                                                                                                                                                                                                                     nitrogen-regulatory protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Ricinus communis"
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BI929601
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BE823431
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CD820903
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CF475242
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BI932123
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AW738071
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BM113473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 4153251521
Bmail: crs@andrew.stanford.edu
Seg primer: T3.
                                                                                BI930336
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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BQ798001 EST 6939
BE239550 EST403599
                                                May 27, 2004, 19:07:55; Search time 1376.09 Seconds (without alignments) 12890.278 Million cell updates/sec
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1 CGSCACGAGGCTACTGCGAA......CTGACATGAGTACTTCTGCT 594
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                                                                                                                                                55026578
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                 - nucleic search, using sw model
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                                  OM nucleic
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B1930336 ESTESCO25
B1930050 ESTESCO25
B193060 ESTESCO25
BM113473 ESTESCO25
BM13473 ESTESCO09
BM92954 ESTESCO09
B1929601 ESTE9499
BES2341 GM700019B
C81819 C81819 Citr
BJ57366 ESTE949383
BES23411 GM700109B
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BJ57366 ESTE9600
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CB3459913 CABZSGO00
CB3459913 CABZSGO00
CB3459913 RTPM2-3-4

USA

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9740 Red Spring Road, Mountain Grove, MO 65711-2999,
Tel: 417 926 4105
Fax: 417 926 6646
Email: weq070f@emsu.edu
                    Southwest Missouri State University-Mountain Grove
                                                                                                        Insert Length: 782 Std Error: 0.00
Plate: VAM-Baker-1-12 row: F column:
Seq primer: T3 PRIMER
High quality sequence stop: 782
POLYA=No.
                                                                                                                                                                                                                                   /organism="Vitis aestivalis"
                                                                                                                                                                                                                                                                                       /db_xref="taxon:3605"
/clone="V-B-112F06"
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Norton"
   Department of Fruit Science
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                                                                                 Poly(A) + RNA was purified from developing stage_III to Poly(A) + RNA was purified from developing stage_III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. cDNA was synthesized and cloned into lambdazAPII according to the instructions of the manufacturer (Stratagene): synthesis was primed from the poly(A) tail, and cloned directionally into NoI (3') and Eccli (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB289081 782 bp mRNA linear EST 27-FEB-2003 V-B-112F06 VAN-Baker-1 Vitis aestivalig CDNA clone V-B-112F06 5', mRNA sequence.
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1 (bases 1 to 782)

Hou, H. S., Phanismth, T. V., Kovacs, L. and Qiu, W. P.

Expressed sequence tags of young leaf tissues of a disease-reastant Vitis aestivalis var. Norton

Compublished (2003)

Contact: Wenping Qiu
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/note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Vector rank" / note="Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE239550 S97 bp mRNA linear EST 12-JUL-2000
EST403599 MHRP- Medicago truncatula cDNA clone pMHRP-28F3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
363 AGGACTGGAGAGATTGGTGATGGCAAGATCTTTTTGGTGCCCATATCGGATGTGATAAGA 304
                                                                                                              523 GTCCGCACTGGTGAGCGGGGTGATAAGGCTGAGAGGATGACAGGAGGGGGGATCTGACATG 582
                                                                                                                                                                                303 crrceatocercarcarcarcarcarcacrescreacearcacearcacearcarcarare 244
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rogids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison,M.J., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Flot,I.E., Cho,J. and Fraser,C.M.
ESTs from phosphate-starved roots of Medicago truncatula
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 ACTGCGAAACTGGGCTTGCTCACTCCTTTCAATAACATCAAGAAGAATTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
1510 San Soble Parkway, Ardmore, OK 73401, USA
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Samuel Noble Roberts Foundation: N265417e TIGR sequence name: MTHAC26TK More information is available at. http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gcg gAT CC). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/mol type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="phosphate-starved"
/lab_host="XIOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula (barrel medic)
Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone lib="MHRP-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Maria J. Harrison
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Best Local Similarity 71.89
Matches 407; Conservative
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                                                                                                                                                                                                                                                  583 AGTACTIC 590
                                                                                                                                                                                                                                                                                                                        243 TCCACTAC 236
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/fore lib="Ripening Grape berries Lambda Zap II Library"
/fore lib="Ripening Grape berries Lambda Zap II, Site 1: Eco
RI, Site 2: XhoI, Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"
                                        EST 30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 723)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CICAAAGAITCICGAAAITICCAGITITAAITIGIGCCIAAACGCICAAAGAAIGGAICI 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AIGGGIAITCGIGGIGITACTGITTCTGAIGTCCGGGGCTTTGGTGCTCAAGGCGGTTTG 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 CCTGAAAGACAGGCAGGCTCTGAATTTTCTGAGGACAAATTTGTTGCTAAAGTCAAAATG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATCGTGGTTAGCAAAGACCAGGTTGAGGATGTTATAGAAAAATCATTGAGGAGGCA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 GAGATTGTGGTGAGCAAAGACCAGGTTGAAGCAGTAATTGACAAGATCAATGAGGTGGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AGAACTGGAGAGATTGGAGACGGCAAGAITTTCTTGCTGCCTGTTTCAGATGTAATAAGA 522
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EST 6939 Ripening Grape berries Lambda Zap II Library Vitis
Vinifera CDNA clone RT093C02 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Pel: 00-33-(0)4-99-61-20-62
Fax: 00-33-(0)4-99-61-20-57
Email: romieu@ensam.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Shiraz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:29760"
/clone="RT093C02"
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Matches 371; Conservative
                                                                                                                                                                                                                                               Vitis vinifera
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BQ798001/c
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from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. CDNA was prepared from poly4+enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA922829 B12 bp mRNA linear EST 09-MAY-2003
EST640547 MTUS Medicago truncatula cDNA clone MTUS-58H7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GITITIGALTITCAGITIGICCAGAGCITAGACALTCTCGGTTTTCTCACTTTAAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TTTTCAAGCTTCAGCGTCATTCGCAAGCGTTTCGGAGATTC-----TTCTCATCGCAAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GIGSTCCTABABAGCAACGGAAATGCATCGATTCTTCCCAAAATCAGAGCTCAAAACCTT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 ATTGCGAAACGGAAGGTGTTGATTTTCATATCAATGAAACCGAATTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 GICTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTCTGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 Arcccrcaedrircrrceserrierreaaaneseaarrcereererekreiarrensar
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                                                                                                                                                            fclone lib="GESD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2
XhoI; Immature seeds, collected from pods ranging in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ACTGCGAAACTGGGCTTGCTCCTCCTTCATTCTAATAACATCAAGAAGAATTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                   /clone="pGESD9J4"
/tissue type="immature seeds"
/dev stage="Immature seeds, 11 to 19 days after
pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.3%; Score 298.6; DB 12; Length 714; llarity 71.8%; Pred. No. 4.7e-72; Conservative 0; Mismatches 154; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGGATGACAGGAGGGCGATCTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 GAGAGGATGGCTGGGGACTAACTGAC 587
  /mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
407; Conserv
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                 ACCGCGGTCAAGCGCGTAAGATATGCCCCCGTCGTTCCTGTGATTAATGCCCAAAGCTCG 192
                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                        GTTTTTGATTTCAGTTTGTTTTGTCCAGAGCTTAGACATTCTCGGTTTTCTCACTTTAAC 132
                                                                                                                                                                                                             GTGGTCCTAAAAAGCAACGGAAATGCATCGATTCTTCCCAAAATCAGAGCTCAAAACTT 2011
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ESTs from developing reproductive tissues of Medicago truncatula
ATTGCGAAACCGAACGTGTTCAACGGTTTGAATTTTCATATGAAACTCAATTTCCT
                                                                                                                   88 ITTTCAAGCTTCAGCGTCATTCGCAAGCGTTTCGGAGATTC-----TTCTCATCGCAAT
                                                                                                                                                                                                                                                                                                        CCTGACTATGTTCCTGAATCCAAGTTTTACAAAGTTGAAGCCATTCTCAGGCCATGGAGA
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1100 Bates Street, Houston, TX 77030-2600,
Tel: 713-798-7044
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leg primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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B397927e
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ORGANISM
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BI311072
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260

86

312

320

372 380

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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
dev_stage="Cell suspensions were subcultured every 14
/clone_lib="Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bell, C.J.,
                                          373 GAAGACAAGITIGITGCTAAAGITAAGATGGAGATCGTGGTTAGCAAAGACCAGGITGAG 432
                                                                                          414 GAAGACAATTITIGITIGCCAAAGITAAAATGGAAATAGTGGTGAGAAAAGACCAGGTTGAG 355
                                                                                                                                                                                                         354 GCAGTGATAAACAAAATTATGGAGACGGCAAGAACTGGGGAGATTGGTGATGGCAAAAATT 295
                                                                                                                                                                                                                                                                                                 Medicago truncatula {barrel medic}
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 ATTGGGAAACGAACGTGTTCAACGGTTTTGAATTTTCAAACTCAAACTCAATTTCCT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF645522 612 bp mRNA linear EST 20-DEC-;
NF036F08EC1F1074 Elicited cell culture Medicago truncatula cDNA
clone NF036F08EC 5', mRNA sequence.
                                                                                                                                                   433 GATGITATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGTTGGAGACGGCAAGATT
                                                                                                                                                                                                                                                            493 ITCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGGGGGGGTGATAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7380
Fax: 580 221 7380
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/mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: radizon@noble.org
Insert Length: 612 Std Error: 0.00
Pusert .056 row: F column: 08
Seg primer: TCACAGGABACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                               234 GAGAGGATGCTGGGACTAACTGAC 208
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/clone lib="MTUG"
/note="Vector: pBluescript SK-; Site_I: EcoRI; Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOIR cells."
                                                                            Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                          VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheurg, F. and Fraser, C.M.

The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries
Unpublished (2002)

Contact: VandenBosch K
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Plant Biology
University of Minnesota
208 BioScil Center, 1445 Gortner Ave, St. Paul, MN 55108, 1
Tel: 612 624 2755
Fax: 612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alias Clone pMARP-28F3
TIGR sequence name: MTUCF91TV
More information is available at: www.medicago.org
Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
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/dev_stage="various stages"
/lab_host="XLOLR"
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/cultivar="A17"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (Dases I to 711)
Van der Hoeven, R.S.; Bezzerides, J.L.; Karamycheva, S.A.; Tsai, J.,
Witterback, T., Van Aken, S., Ronning, C.M.; Nierman, W., Fraser, C.M.;
Martin, G.B.; Giovannoni, J.J. and Tanksley, S.D.
                                                                                                                                                                                                                                                                                                                                                                                           297
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Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 GGCTCCGAATTTTCAGAAGACAATTTTGTTGCCAAAGTTAAAATGGAAGTAGTGGTGGGA
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/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA ogenerated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
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                                                                                                                     DB 14; Length
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Pred. No. 6.3e-66;
0; Mismatches 124; Indels
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Clemson University Genomics Institute
Clemson University
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Best Local Similarity 73.9%;
Matches 351; Conservative
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           GTTTTTGATTTCAGTTTGTTTTGTCCAGAGCTTAGACATTCTCGGTTTTCTCACTTTAAC 132
                                                                                                                                          GTGGTCCTAAAAAGCAACGGAAATGCATCGATTCTTCCCAAAATCAGAGCTCAAAACCTT 217
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                                                   104 TTTTCAAGCTTCAGCGTCATTCGCAAGCGTTTCGGAGATTC-----TTCTCATCGCAAT 157
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Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                       CCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGA
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University of Missouri
1D8 Waters Hall, Columbia,
TP1: 573-884-4752
Fax: 573-882-0588
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Single pass sequence
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Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamids, Lamiales, Antirrhinaceae, Antirrhineae,
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2 achdgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
                                                                   /tissue type="flower"
/dev stage="buds 8mm to preanthesis"
/dow stage="buds 8mm to preanthesis buds"
/clone lib="tomato flower. 8 mm to preanthesis buds"
/rone="Vector: pBluescript SK(-); Site_1: BcoRI; Site_2:
KroI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                   175 CACCTICAAACGCTGTCAAAATGCTCCTTTCCCGATTATCAGAGCCCAAAACTCTCC
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                                                                                                                                                                                                                                                                                  46.3%; Score 275.2; DB 1.75.9%; Pred. No. 1.5e-65;
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clone="cTOC22H10"
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mol_type="mRNA"
cultivar="TA496"
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D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liano,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B.
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 GITCCTGIGATTAATGCCCAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                               Length 732;
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/tiseuc_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                95; Indels
                                                                                                                                                                                                                                                                                                                                                               Score 275; DB 9;
Pred. No. 1.7e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
   Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                               /organism="Antirrhinum
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               46.3%;
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/culcivar="TA496"
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/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AGACAAGITIGITGCIAAAGITAAGAIGGAGAICGIGGITAGCAAAGACCAGGITGAGGA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 CACCTTCAAACGCTGTCAAAATGCTCCTTCTTTCCGATTATCAGAGCCCAAAACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 TCGTGSTTTTGGCCCCAAGGTGGCTTGACTGAGGCAAGCTGGCTCTGAATTCTCTGAA
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Generation of ESTs from tomato callus tissue Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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JOURNAL
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                                                                                                                                                                           /mol_type="mkNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /close lib="tomato resistant, Cornell" /close lib="tomato resistant, Cornell" /cote="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2: Xho1: clER - Tomato Pseudomonas Resistant EST library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRl and 3' end with Xhol site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCGGTCAAGCGCGCTAAGATATGCCCCCCGTCGTTCCTGTGATTAATGCCCCAAAGCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AGATTTCGTCCCTGATGCGAAGTTTTACAAAGTTGAAGCAATTCTAAGACCTTGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TCAACAGGTTTCTTCGGCACTACTGAAATGGGCATTCGTGGTGTCACTGTTTCGGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 274.2; DB 9; Length 648; 75.7%; Pred. No. 2.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 109; Indels
                                                                                                                                       'organism="Lycopersicon esculentum'
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                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                /db xref="taxon:4081"
/clone="clerse12"
                                                 Location/Qualifiers
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                                                                     EST 18-OCT-2001
                                                                                                                                                                                                                                                    Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; laminids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 736)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
van der Hoeven, R.S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemeon University
100 Jordan Hall, Clemson, SC 29634, USA
Bmail: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGGTCAAGCGCGTAAGATATGCCCCCGTCGTTCCTGTGATTAATGCCCAAAGCTCGCC
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                                                                  BI932913 736 bp mRNA linear EST 18-OCT-EST52802 tomato flower, 8 mm to preanthesis buds Lycopersicon esculentum cDNA clone cTOC24H17 5' end, mRNA sequence.
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46.1%; Score 273.6; DB 12; Length
Best Local Similarity 75.7%; Pred. No. 4.3e-65;
Matches 339; Conservative 0; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="croc22633"
/tissue type="flower"
/dev_stage="buds Bam to preanthesis"
/dev_stage="buds Bam to preanthesis buds"
/clone lib="temato flower, 8 mm to preanthesis buds"
/note="vector: pBluescript SK(-); Site_1: BcoRI; Site_2:
/khol; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taker from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
                   Tracheophyta;
             Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Spermatophyta; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon. (bases 1 to 702) van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Wartin, G.B., Giovannoni, J.J., and Tankeley, S.D. Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AGATTTCGTCCCTGATGCGAAGTTTTACAAAGTTGAAGCAATTCTAAGACCTTGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 CACCTTCAAACGCTGTCAAAATGCTCCTTTTCCCGATTATCAGAGCCCAAAACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 TGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGT
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46.1%; Score 273.6; DB 12; Length 702;
Best Local Similarity 75.7%; Pred. No. 4.3e-65;
Matches 339; Conservative 0; Mismatches 109; Indels 0;
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/mol_type="mRNA"
/culTivar="TA496"
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1. .702
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Unpublished (2001)
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SET339498 : Lomato flower buds, anthesis, Cornell University
Lycopersicon esculentum cDNA clone cTOD5K11 5', mRNA sequence.
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Liang,F., Hansen,T.S., Bezzeredes,J.L., Matern,A.E., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. ESTS from tomato flower tissue, anthesis Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
437 AGTCATTGCCATGATAATTGAAGAGGCAAGAACTGGTGAAATAGGTGATGGAAAGATATT 496
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                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="flower"
/dev_stage="anthesis"
/clone_lib="tomato flower buds, anthesis, Cornell
University"
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Best Local Similarity 75.7%; Pred. No. 4.3e-65;
Matches 339; Conservative 0; Mismatches 109; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Clemson University
100 cordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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/mol_type="mRNA"
/culTivar="TA496"
                                                                                                                      GAGGATGACAGGAGGCGATCTGACATG 582
                                                                                                                                              Lycopersicon esculentum (tomato)
Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:4081"
/clone="cTOD5K11"
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